

FIGURE 1

CCAATGCCCGGTGCGGTGGTGCAGGGTCTCGGGCTAGTC**ATG**GCGTCCCCGTCTGGAGAC
TGCAGACTAAACCAGTCATTACTGTTCAAGAGCGTTCTGCTAATCTACACTTTATTTTC
TGGATCACTGGCGTTATCCTTCTTGCAGTTGGCATTGGGGCAAGGTGAGCCTGGAGAATTA
CTTTCTCTTTAAATGAGAAGGCCACCAATGTCCCTTCGTGCTCATTGCTACTGGTACCG
TCATTATTCTTTGGGCACCTTGGTTGTTGCTACCTGCCAGCTCTGCATGGATGCTA
AAACTGTATGCAATGTTCTGACTCTCGTTTTGGTCGAACGGTCGCTGCCATCGTAGG
ATTTGTTTCAGACATGAGATTAAGAACAGCTTAAGAATAATTATGAGAAGGCTTGAGC
AGTATAACTCTACAGGAGATTATAGAACGATGCAGTAGACAAGATCCAAAATACGTTGCAT
TGTTGTGGTGTCAACGATTATAGAGATTGGACAGATACTAATTACTCAGAAAAAGGATT
TCCTAAGAGTTGCTGTAACCTGAAAGATTGTAACGACTCCACAGAGAGATGCAGACAAAGTAAACA
ATGAAGGTTGTTTATAAAGGTGATGACCATTATAGAGTCAGAAATGGGAGTCGTTGCAGGA
ATTCCTTGGAGTTGCTTCCAAGTGATTGGAATCTTCTCGCCTACTGCCWCTCTCG
TGCCATAACAAATAACCAAGTATGAGATAGT**GTA**ACCAATGTATCTGTTGGCCTATTCTCT
CTACCTTAAGGACATTAGGGTCCCCCTGTGAATTAGAAAGTTGCTTGGCTGGAGAACTG
ACAACACTACTGATAGACCAAAAAACTACACCAAGTAGGTTGATTCAATCAAGATGTAT
GTAGACCTAAAACACCAATAGGCTGATTCAATCAAGATCCGTGCTCGCAGTGGGCTGAT
TCAATCAAGATGTATGTTGCTATGTTCAAGTCCACCTCTATCCCATTGTTAGATCG
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FIGURE 2

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA19902
><subunit 1 of 1, 245 aa, 1 stop, 1 unknown
><MW: -1, pI: 8.36, NX(S/T): 1
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VLIATGTVIILLGTFGCFATCRASAWMLKLYAMFLTLVFLVELVAAIVGFVFRHEIKNSFKN
NYEKALKQYNSTGDYRSHAVDKIQNTLHCCGVTDYRDWTDTNYYSEKGFPKSCKLEDCTPQ
RDADKVNNEGCFIKVMTIIESEMGVVAGISFGVACFQLIGIFLAYCXSRAITNNQYEIV
```

Important features of the protein:

Signal peptide:

amino acids 1-42

Transmembrane domains:

amino acids 19-42, 61-83, 92-114, 209-230,

N-glycosylation site.

amino acids 134-138

Tyrosine kinase phosphorylation site.

amino acids 160-168, 160-169

N-myristoylation site.

amino acids 75-81, 78-84, 210-216, 214-220, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 69-80, 211-222

FIGURE 3

FIGURE 4

MIVFGWAVFLASRSLGQGLLTLEEHIAHFLGTGGAATTMGNSCI
AENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDKO

Signal peptide:

amino acids 1-16

Casein kinase II phosphorylation site.

amino acids 22-26, 50-54, 113-117

N-myristoylation site.

amino acids 18-24, 32-38, 34-40, 35-41, 51-57

FIGURE 5

GGCACGAGGCCTGTCCACCCGGGGCGTGGAGTGAGGTACCAGATTAGCCCATTGGCC
CCGACGCCCTGTTCTCGGAATCCGGGTGCTGCGGATTGAGGTCCCGTTCTAACGGACTG
CAAGATGGAGGAAGGCGGGAACCTAGGAGGCCTGATTAAGATGGTCATCTACTGGTCTTGT
CAGGTGCCTGGGCATGCAAATGTGGGTGACCTTCGTCTCAGGCTTCTGCTTTCCGAAGC
CTTCCCCGACATACCTCGGACTAGTGCAGAGCAAACCTTCCCCTCTACTTCCACATCTC
CATGGGCTGTGCCTCATCAACCTCTGCATCTTGGCTTCACAGCATGCTGGGCTCAGCTCA
CATTCTGGGAGGCCAGCCAGCTTACCTGCTGTTCTGAGCCTACGCTGGCCACTGTCAAC
GCCCGCTGGCTGGAACCCCGCACACAGCTGCCATGTGGGCCCTGCAAACCGTGGAGAAGGA
GCGAGGCCTGGGTGGGGAGGTACCAAGGCAGCCACCAGGGTCCCGATCCCTACCGCCAGCTGC
GAGAGAAGGACCCAAGTACAGTGCTCTCGCCAGAATTCTTCCGCTACCATGGGCTGTCC
TCTCTTGCAATCTGGGCTGCCCTGAGCAATGGGCTCTGTCTCGCTGGCCTTGCCCTGGA
AATAAGGAGCCTCTAGCATGGGCCCTGCATGCTAATAATGCTTCTTCAGAAATGAAAAAAA
AAAAAAAAAAA

FIGURE 6

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<subunit 1 of 1, 231 aa, 1 stop
<NX(S/T): 0
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GCAF INLCILASQHAWAQLTFWEASQLYLLFLSLTLATVNARWLEPRTTAAMWALQTVEKER
GLGGEVPGSHQGPDPYRQLREKDPKYSALRQNFFRYHGLSSLCNLGCVLSNGLCLAGLALEIRSL
```

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 86-103, 60-75

Casein kinase II phosphorylation site.

amino acids 82-86

Tyrosine kinase phosphorylation site.

amino acids 144-151

N-myristoylation site.

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 54-65

G-protein coupled receptors proteins.

amino acids 44-85

FIGURE 7

AATTCA GATTTAAGCCCATTCTGCAGTGGAA TTTCATGA AACTAGCAAGAGGACACCATCTT
 CTTGTATTATA CAAGAAAGGAGTGTACCTATCACACACAGGGGGAAAA**ATG**CTCTTTGGGT
 GCTAGGCCTCCTAATCCTCTGGTTCTGTGGACTCGTAAAGGAAA ACTAAAGATTGAAG
 ACATCACTGATAAGTACATTTTATCACTGGATGTGACTCGGGCTTGGAAACTTGGCAGCC
 AGAACCTTGATAAAAAGGGATTTCATGTAATCGCTGCCTGTCTGACTGAATCAGGATCAAC
 AGCTTAAAGGCAGAACCTCAGAGAGACTTCGTACTGTGCTCTGGATGTGACCGACCCAG
 AGAATGTCAAGAGGACTGCCAGTGGGTGAAGAACCAAGTTGGGAGAAAGGTCTCTGGGT
 CTGATCAATAATGCTGGTGTCCC CGCGTGTGGCTCCACTGACTGGCTGACACTAGAGGA
 CTACAGAGAACCTATTGAAGTGAACCTGTTGGACTCATCAGTGTGACACTAAATATGCTTC
 CTTGGTCAAGAAAGCTCAAGGGAGAGTTATTAAATGTCTCCAGTGGAGGTGCCCTGCA
 ATCGTGGAGGGGCTATACTCCATCCAAATATGCA GTGGAAGGTTCAATGACAGCTTAAG
 ACGGGACATGAAAGCTTTGGTGTGCACGTCTCATGCATTGAACCAGGATTGTTCAAAACAA
 ACTTGGCAGATCCAGTAAAGTAATTGAAAAAAACTGCCATTGGAGCAGCTGTCTCCA
 GACATCAAACAACAAATATGGAGAAGGTTACATTGAAAAAAAGTCTAGACAAACTGAAAGGCAA
 TAAATCCTATGTGAACATGGACCTCTCCGGTGGTAGAGTGCATGGACCACGCTCTAACAA
 GTCTCTCCCTAAGACTCATTATGCCGCTGGAAAAGATGCCAAATTTCTGGATA CCTCTG
 TCTCACATGCCAGCAGCTTGCAAGACTTTATTGTTGAAACAGAAAGCAGAGCTGGCTAA
 TCCCAAGGCAGTG**TGA**CTCAGCTAACCAAAATGTCTCCTCCAGGCTATGAAATTGGCCGAT
 TTCAAGAACACATCTCCTTCAACCCATTCTTATCTGCTCCAACCTGGACTCATTAGA
 TCGTGCTTATTGGATTGCAAAAGGGAGTCCCACCATCGCTGGTGGTATCCCAGGGCCCTG
 CTCAAGTTCTTGAAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCCTGCCCTGT
 ATTAGGCTTGCCTGCTGGTGTGATGTAAGGAAATTGAAAGACTTGCCCATTCAAATG
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 AAAAAAAAAAAAAAA

FIGURE 8

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LTLEDYREPIEVNLFGLISVTLNMLPLVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGF
NDSLRRDMKAFGVHVSCTIEPGLFKTNLADPVKVIEKKLAIWEQLSPDIKQQYGEFYIEKSLD
KLKGNKSYVNMDLSPVVECMDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLLKQK
AELANPKAV
```

Important features of the protein:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 136-152

N-glycosylation sites.

amino acids 161-163, 187-190 and 253-256

Glycosaminoglycan attachment site.

amino acids 39-42

N-myristoylation sites.

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

FIGURE 9

GCGGGCTGTTGACGGCGCTGCG**ATG**GCTGCCTGCGAGGGCAGGAGAACGGAGCTCTCGGTT
CCTCTCAGTCGGACTTCCCTGACGCCGCCAGTGGCGGGGCCCTTGGCCGTCGCCACCACT
GTAGTCATGTACCCACCGCCGCCGCCCTCATCGGACTTCATCTCGGTGACGCTGAG
CTTGCGAGAGCTATGACAACAGCAAGAGATTGGCGGCCGCTCGTGGAGGAAATGGAA
AGCAACTGTCGAGATTGCAGCGGAATATGATTCTCTCCTTGCCTTCTGCTTTCTGT
GGACTCCTCTTACATCAACTTGGCTGACCATTGAAAGCTCTGGCTTTCAGGCTAGAGGA
AGAGCAGAAGATGAGGCCAGAAATTGCTGGGTAACACCAGCAAATCCACCCGCTTACCAAG
CTCCTCAGAAGGCCACCGACCTGAGAACATTACCTGAGATTGACGATTCGTACAGAAGACACAA
AGACACATCCAGCAGGGGACCACCTCACCTGAGATTAGACCCCCAAGCCAAGACCTGAAGGA
TGGGACCCAGGAGGAGGCCACAAAAGGCAAGAAGCCCCTGTTGGATCCCCGCCAGGAG
ATCCGAGAGGACAGTCATCAGCTGGAGGGAGCGGTGATCGAGCCTGAGCAGGGCACCGAG
CTCCCTCAAGAAGAGCAGAAGTGCCACCAAGCCTCCCTGCCACCGGCCAGGACACAGGG
CACACCAGTGCATCTGAACTATGCCAGAAGGGCGTGAAGTGCCTTCATGCATGGAA
AAGGATACCGCAAGTTGCATGGGCCATGACGAGCTGAAGCCTGTTGAGGTCTTCAAGT
GAGTGGTTGGCTCGGTCTCACACTGATCGACGCCGCTGGACACCATTGGATCTGGGTCT
GAGGAAAGAATTGAGGAAGCCAGGAAGTGGGTGTCAGAAAGTTACACTTGAAGGACG
TGGACGTCAACCTGTTGAGAGCACGATCCGCATCCTGGGGGGCTCTGAGTGCCTACAC
CTGTCGGGACAGCCTTCTGAGGAAGCTGAGGATTGGAAATCGGCTAATGCCTGC
CTTCAGAACACCATCCAAGATTCTTACTCGGATGTGAACATCGGTACTGGAGTTGCCACC
CGCCACGGTGGACCTCCGACAGCACTGTGCCGAGGTGACCAGCATTAGCTGGAGTTCCGG
GAGCTCTCCGCTCACAGGGATAAGAAGTTCAGGAGGCAGTGGAGAAGGTGACACAGCA
CATCCACGGCTGTCTGGAAAGAAGGATGGCTGGCCATGTCATCAATACCCACAGTG
GCCTCTCACCCACCTGGCGTATTCACGCTGGGCCAGGGCGACAGCTACTATGAGTAC
CTGCTGAAGCAGTGGATCCAGGGCGGGAAAGCAGGAGACACAGCTGTTGGAGACTACGTGG
AGCCATCGAGGGTGTCAAACGCACCTGCTGCCACTCCGAGGCCAGTAAGCTCACCTTG
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GGGACGCTGGCTCTGGCGTCTACCACGGCTGCCAGGCCACATGGAGCTGGCCAGGA
GCTCATGGAGACTTGTACAGATGAACCGCAGATGGAGACGGGGCTGAGTCCGAGATCG
TGCACCTCAACCTTACCCCCAGCCGGCCGTCGGACGTGGAGGTCAGCCAGCACAGG
CACAAACCTGCTGCCAGAGACCGTGGAGAGCCTGTTACCTGTACCGCGTACAGGGGA
CCGCAAATACCAGGACTGGGCTGGAGATTCTGCAAGACTCAGCCGATTACACGGGTCC
CCTCGGGTGGCTATTCTCCATCAAACATGTCCAGGATCCTCAGAAGCCCAGCCTAGGGAC
AAGATGGAGAGCTTCTCCTGGGGAGACGCTCAAGTATCTGTTCTGCTCTCCGATGA
CCCAAACCTGCTCAGCCTGGACGCCACGTGTTCAACACCGAAGCCCACCCCTGCCTATCT
GGACCCCTGCC**TAG**GGTGGATGGCTGCTGGTGTGGGACTTCGGGTGGCAGAGGCACCTTG
CTGGGTCTGTGGCATTTCAGGGCCACGTAGCACCAGCAACGCCAGTGGCCAGGGCT
CTGAACCTGGCTCTGGCTCCTCGTCTGCTTAATCAGGACACCGTGGAGGACAAGTGA
GCCGCTCAGTCTGGTGTGATGCCGGTGGCTGGCCGCTGGAGCCTCCGCTGCTTCCTC
CAGAAGACACGAATCATGACTCACGATTGCTGAAGCCTGAGCAGGTCTCTGTGGCCGACCA
GAGGGGGCTCGAGGTGGTCCCTGGTACTGGGGTGACCGAGTGGACAGCCCAGGGTGCAGC
TCTGCCGGCTCGTGAAGCCTCAGATGTCCCCAATCCAAGGGCTGGAGGGCTGCCGTGA
CTCCAGAGGCCTGAGGCTCCAGGGCTGGCTCTGGTGTGAGGACTCAGGGATCCTC
CTGGCCGCCCGCAGGGGCTGGAGGGCTGGACGGCAAGTCCGTCTAGCTCACGGGCC
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FIGURE 10

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><subunit 1 of 1, 699 aa, 1 stop
><MW: 79553, pI: 7.83, NX(S/T): 0
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IAGLK PANPPVLPAPQKADTDPENLPEISSQKTQRHIQRGPPHLQIRPPSQDLKDGTQEEAT
KRQEAPVDPRPEGDPQRTVISWRGAVIEPEQGTEPLPSRRAEVPTKPLPPARTQGTPVHLNY
RQKGVIDVFLHAWKGYRKFAWGHDELKPVSRSFSEWFGLGLTLIDALDTMWILGLKEFEEA
RKWVSKKLHFEKDVDVNLFESTIRILGGLLSAYHLSGDSLFLRKAEDFGNRLMPAFRTPSKI
PYSDVNIGTGVAHPPRWTSDSTVAEVTISIQLEFRELSRLTGDKKFQEAVEKVTOHIHGLSGK
KDGLVPMFINTHSGLFTHLGVFTL GARADSYYEYLLQWIQGGQETQLEDYVEAIEGVRT
HLLRHSEPSKLTFGELAHGRFSAKMDHLVCFLPGTLALGVYHGLPASHMELAQELMETCYQ
MNRQMETGLSPEIVHFNLYPQPGRRDVEVKPADRHNL RPETVESLFYLYRVTGDRKYQDWG
WEILQSFSRFTRVPSGGYSSINNVQDPQKPEPRDKMESFFLGETLKYLFLFSDDPNLLSLD
AYVFNTEAHPLPIWTPA
```

Important features of the protein:

Transmembrane domain:

amino acids 21-40 and 84-105 (type II)

FIGURE 11

GGCGCCGCGTAGGCCGGAGGCCGGCCGGCTGCGAGGCCCTGCCCATGCGCCGC
 CGCCTCTCCGCACG**ATG**TTCCCCTCGCGGAGGAAAGCGGCCAGCTGCCCTGGGAGGACGGC
 AGGTCCGGGTTGCTCTCCGGCCCTCCCTCGGAAGTGTTCGTCTCCACCTGTTGTGGC
 CTGCCTCTCGCTGGGCTTCTTCTCCCTACTCTGGCTGCAGCTCAGCTGCTCTGGGGACGTGG
 CCCGGCAGTCAGGGACAAGGGCAGGAGACCTCGGGCCCTCCCCGTGCCTGCCCTGGCAGTGCTGGT
 CCGCCCCCTGAGCACTGGGAAGAAGACGCATCCTGGGGCCCCACCGCCTGGCAGTGCTGGT
 GCCCTTCCCGAACGCTTCGAGGAGCTCCTGGTCTCGCCCCACATGCGCCGCTTCCTGA
 GCAGGAAGAAGATCCGGCACCATCTACGTGCTCAACCAGGTGGACCACCTCAGGTTCAAC
 CGGGCAGCGCTCATCAACGTGGGCTTCTGGAGAGCAGAACAGCACGGACTACATTGCCAT
 GCACGACGTTGACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTCCTGAGGCTGGC
 CCTTCCACGTGGCCTCCCCGGAGCTCCACCCCTCTACCAACTACAAGACCTATGTCGGCGGC
 ATCCTGCTGCTCTCCAAGCAGCACTACCGGCTGTGCAATGGATGTCCAACCGCTTCTGGG
 CTGGGGCCGCGAGGACGACGAGTTCTACCGGCGATTAAGGGAGCTGGCTCCAGCTTTCC
 GCCCTCGGAATACAACACTGGGTACAAGACATTGCCCCCTGCATGACCCAGCCTGGCG
 AAGAGGGACCAGAACGCGATCGCAGCTAAAAACAGGAGCAGTTCAAGGTGGACAGGGAGGG
 AGGCCTGAACACTGTGAAGTACCATGTGGCTCCCGACTGCCCTGTCTGTGGCGGGCCC
 CCTGCACTGTCCTAACATCATGTTGGACTGTGACAAGACGCCACACCCTGGTGCACATT
 AG**TGA**GCTGGATGGACAGTGAGGAAGCCTGTACCTACAGGCCATTGCTCAGGCTCAGGA
 CAAGGCCTCAGGTCGTGGCCAGCTCTGACAGGATGTGGAGTGGCCAGGACCAAGACAGCA
 AGCTACGCAATTGCAGCCACCCGGCCAAAGGCAGGCTGGCTGGCCAGGACACGTGG
 GTGCCCTGGGACGCTGCTGCCATGCACAGTGATCAGAGAGAGGCTGGGTGTCCCTGTCCG
 GGACCCCCCCTGCCTCCTGCTCACCTACTCTGACCTCCTCACGTGCCAGGCCTGTGG
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FIGURE 12

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GQQQETSGPPRACPPEPPPEHWEEDASWGPRLAVLVPFRERFEELLVFVPHMRRFLSRKKI
RHIIYVLNQVDHFRFNRAALINVGFLESSNSTDYIAMHDVDLLPLNEELDYGFPEAGPFHVA
SPELHPLYHYKTYVGGILLLSKQHYRLCNGMSNRFWGWGREDDDEFYRRIKGAGLQLFRPSGI
TTGYKTFRHLHDPAWRKRDQKRIAAQKQEKFVDRREGGLNTVKYHVASRTALSVGGAPCTVL
NIMLDCKTATPWCTFS
```

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 29-49 (type II)

N-glycosylation site.

amino acids 154-158

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 27-31

Tyrosine kinase phosphorylation site.

amino acids 226-233

N-myristoylation site.

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

FIGURE 13

CAATTTGCCTATCCACCTCCCCAAGCCCCTTACCT**ATG**GCTGCTGCTAACGCTGCTGCT
GCTGCTGCTGCTAAAGGCTCATGCTTGGAGTGGGACTGGTCGGTGCCAGAAAGTCT
CTTCTGCCACTGACCCCCATCAGGGATTGGGCCTCTTCCCCCTCCTTCTGTGTCTC
CTGCCTCATCGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGAAGGGGAGAAAGT
GGGGGATGGC**TAA**GAAAGCTGGAGATAGGAACAGAACAGGGTAGTGGGTGGCTAGGGGG
GCTGCCTTATTAAAGTGGTTGTTATGATTCTTATACTAATTATAAAAGATATTAAGGC
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FIGURE 14

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PRGEGEKVGDG
```

Important features:

Signal peptide:

amino acids 1-15

Growth factor and cytokines receptors family:

amino acids 3-18

FIGURE 15

GGGACCCATGCGGCCGTGACCCCCGGCTCCCTAGAGGCCAGCGCAGCCGCAGCGGACAAAG
 GAGCATGTCCGCGCCGGGAAGGCCCGTCCCTCCGGCCGCATAAGGCTCCGGTCGCCGCTGG
 GCCCGCGCCCGCCTGCCGCCCAGGGCTCCGGGCCGCTAGGCCAGTGCGCCGCG
 CTCGCCCCGCAGGCCGGCCGCAGCAGCAGGAGGCCACCCGGACGCCGGCGGGCCGCGCA
 GCCGCCGCTGTTGCTGCCGCTCGCTGTTAGCGCTGCTCGCCTGCTGGGAGGCAGGGCG
 GCGGCCGGCGCCGCCGCGCTGCCGCCGGCTGCAAGCACGATGGGCCGGCCCCGAGGGCTGGC
 AGGGCGGCCGGCGCCGCCGAGGGCAAGGTGGTGTGCAGCAGCCTGGAACTCGCGCAGGTCT
 GCCCCCAGATACTCTGCCAACCGCACGGTACCCCTGATTCTGAGTAACAATAAGATATCCG
 AGCTGAAGAATGGCTCATTTCGGGTTAAGTCTCCTGAAAGATTGGACCTCGAAACAAT
 CTTATTAGTAGTATAGATCCAGGTGCCTCTGGGACTGTCATCTCTAAAAAGATTGGATCT
 GACAAACAATCGAATAGGATGTCAGACATGCAAGACATATTCGAGGACTCACCAATCTGGTTC
 GGCTAAACCTTCGGGAATTGTTCTTCATTATCTCAAGGAACCTTGATTATCTGCG
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 GCATCGCTGGTAAAGGAGAACATCACGGTACGGGATACCAGGTGTGTTATCCTAAGT
 CACTGCAGGCCAACCAACCAGTCACAGGCGTGAAGCAGGAGCTGTTGACATGCGACCCCTCCGCTT
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 TCCCTTCCAGTGCATGGCTCATATATTGATCAGGACATGCAAGTGTGTTGATCAGGATG
 GGAGAAATAGTTGAAACCGATGAATCGCAAGGTATTTGTTGAAAAGAACATGATTACAAC
 TGCTCCTTGATTGCAAGTGCCTTAACCATTTCAATATTCAGGCTGGATCTACTGAAATTG
 GGGCTGTATGTCCAGACCAAACGTGGAATAATACGAGGACTGTGGATATTGTGGTATTAG
 AGAGTTCTGCACAGTACTGTCCTCCAGAGAGGGTGGTAAACAACAAAGGTGACTTCAGATGG
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 GATATATCCGGAAACCCACAGGATGAGAGAAAAGCTTGGCGCAGATGTGATAGAGGTGGCT
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 TTGAAAATTTGGAAGATTACCAAGGAGGAAAATCAAAGAGCTAGGTGACGTGATGGTT
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 ACTTCCGGATTATGGGAGGCGGGATCCAGAGGGAAACCTGGATAAGCAGCTGAGCTTAAAGT
 GCAATGTTCAAATACATTTCGAGTCTGGCACTAAAGGTATGTCATTCTGCAATCATT
 AAGACTATTACAGT**TAA**ATTAGAATGCTCAAATGTTCTGCTCGAAAATAACCTTATT
 AAAGATTTTTTGCAAGGAAGATAGGTATTATTGCTTTGCTACTGTTAAAGAAAACAA
 ACCAGGAAGAACTGCATTACGACTTCAAGGGCCCTAGGCATTGCTTGCCTTGATTCCCTT
 CTTCACATAAAATATCAGAAATTACATTACTGCAGTGGTATAATGCAAATAACT
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 GATTTAAGACAATAAGATGTTTCATGGGCCCTAAAGTATCATGAGCCTTGGCACTGC
 GCCTGCCAACGCTAGTGGAGAAGTCACCCCTGAGACCAAGGTGTTAATCAAGCAAGCTGAT
 ATCAAAATTGCAAGGAAACAAATATGTCATATCTTTTTAAAGTATTCA
 TTGAAGCAAGCAAATGAAAGCATTGACTGATTAAATTGCTTAAAGGAGGAGGACAACTCCAG
 GACTACACTGTATTGAAAGCAAATAGAGGAGGACAAACTCCAGCACCCCTAATGGAACCACATT
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 TACTTATTCTGCTTGTCCCTCAATAATATCACAAACAATATCCAGTCATTAAATGGC
 TGCATAATAACTGATCCAACAGGTGTTAGGTGTTAGTGTGAGCACTCAATAAATA
 TTGAATGAATGAACGAAAAAAAAAAAAAA

FIGURE 16

MEPPGRRRGRAQPPLLPLSLLALLGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGK
VVCSSLELAQVLPPDTLPNRTVTLLSNNKISELKNGSFSGLSLLERLDLRNNLISSIDPGA
FWGLSSLKRDLTNNRIGCLNADIFRGLTNLVRNLSGNLFSSLSQGTFDYLASLRSLEFQT
EYLLCDCNILWMHRWVKEKNITVRDTRCVYPKSLQAQPVTGVVKQELLTCDPPELPSFYMTP
SHRQVVFEGDSLFPQCMASYIDQDMQVLWYQDGRIVETDESQGIFVEKNMIHNCSLIASALT
ISNIQAGSTGNWGCHVQTKRGNNRTVDIVVLESSAQYCPPERVNNKGDFRWPRLAGITA
YLQCTRNTHGSGIYPGNPQDERKAWRRCDRGGFWADDYSRCQYANDVTRVLYMFNQMPLNL
TNAVATARQLLAYTVEAANFSDKMDVIFVAEMIEKFGRTKEEKSKELGDVMVDIASNIMLA
DERVLWLAQREAKACSRIVQCLQRIATYRLAGGAHVYSTYSPNIALEAYVIKSTGFTGMTCT
VFQKVAASDRTGLSDYGRRDPEGNLDKQLSFKCNVSNTFSSLALKVCYILQSFKTIYS

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 13-40 (type II)

N-glycosylation site.

amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336,
433-437, 453-457, 592-596

N-myristoylation site.

amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57,
57-63, 99-105, 123-129, 142-148, 162-168, 317-323, 320-326,
384-390, 403-409, 554-560

FIGURE 17

GC GTGGGG**ATG**TCTAGGAGCTCGAAGGTGGT GCTGGGCCTCTCGGTGCTGCTGACGGCGGCC
ACAGTGCCGGCGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTAT
CAGAGACATTGAGAGGCAAATTGGAAAAAGAAAACATT CGTCTTTGGGAGAACAGATTA
TTTGACTGAGCAACTTGAAGCAGAAAGAGAGAAGATGTTATTGGCAAAAGGATCTCAAAAAA
TCATGACTTGAATGTGAAATATCTGTTGGACAGACAACACAGAGTTGTGTGTGTTGAT
GGAGAGTAGCTTAGTGTATCTTCATCTTTGGTCACTGTCCTTTAAACTGATCA
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GTGTGGGCAGACACTTTGGAAAGAGTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGG
TCACTGTCCAGTGCTTAGGGTTACTGAGAAGCACTGCCGAGCTTGTGAGAAGGAAGGGA
TGGATAGTAGCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAAC
TCGACCTCAGAAGGACTGGAGGAAGGTGAAGTGGAGGGAGAGACGCTCCTGATCGTCGAATCC

FIGURE 18

MSRSSKVVLGLSVLTAATVAGVHVKKQQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIILT
EQLEAEREKMLLAKGSQKS

Signal peptide:

amino acids 1-21

FIGURE 19

CTGTCGTCTTGCTTCAGCCGCAGTCGCCACTGGCTGCCAGGGTGCCTACAGCCTGTT
 CAAGTGTGGCTTAATCCGTCTCCACCACCAAGATCTTCTCCGTGGATTCCCTCTGCTAAGACC
 GCTGCCATGCCAGTGACGGTAACCCGCACCACCATACAACCACGACGTATCTCGGG
 CCTGGGGTCCCCCATGATCGTGGGGTCCCCTCGGGCCCTGACACAGCCCCTGGGTCTCCTCGC
 CTGCTGCAGCTGGTGTCTACCTGCCTCGCTGGTAGCGTGGCGCTGGAC
 GGGGTCCATGGGCAACTGGTCCATGTTCACCTGGTGCTCTGCTCTCCGTGACCGTGTAC
 TCCTCATCGTGGAGCTGTGCAGGCTCCAGGCCGCTTCCCCCTGTCTGGCGAACCTCCCC
 ATCACCTTCGCCTGCTATGCCGCCTCTCGCTCTGGCCTCCATCATCTACCCAC
 CTATGTCCAGTCCTGTCCCACGGCCGTTGCGGGACCACGCCATGCCGCCACCTCTCT
 CCTGCATCGCGTGTGGCTTACGCCACCGAAGTGGCCTGGACCCGGCCGGCGAG
 ATCACTGGCTATATGCCACCGTACCCGGCTGCTGAAGGTGCTGGAGACCTCGTGCCTG
 CATCATCTCGCGTTACGCCATCTGCTTACGCCATCGCTGCTGAACCTGGGG
 GCGTGGCGGTGTACGCCATCTGCTTACGCCATCGCTGCTGAACCTGGGG
 GAGTGCACCAACGTGCTACCCATCCCCCTCCCCAGCTTCTGTGGGGCTGGCCTGTC
 TGTCTCCTCTATGCCACGCCCTGTTCTGGCCCTCTACCAGTTGATGAGAAAGTATG
 GCAGGCCAGCCTCGCGCTCGAGAGATGTAAGCTGCAGCCGCAGCCATGCCCTACTACGTGT
 GCCTGGGACCGCCGACTGGCTGTGGCCATCCTGACGCCATCACCTACTGGGTATGTGG
 TGACCTGGTGCACTCTGCCACCTGGTTTGTCAGGTCTAAAGACTCTCCAAGAGGCTCC
 CGTTCCCTCTCCAACCTCTTGTCTTGTGCCCCAGTTTCTTATGGAGTACTTCTTCC
 TCCGCCTTCCTCTGTTCTCTGCCCTCCCTGTCTCCCTCCACCTTTCTTCCCT
 CAATTCCCTGCACTCTAACCAAGTTCTGGATGCATCTCTCCCTTCCCTTGCTGT
 TTCCCTCCTGTGTTGTTGTTGCCACATCCTGTTCAACCCCTGAGCTGTTCTCTT
 CTTTCTTCTTTTTTTTTTTTAAGACGGATTCTCACTCTGTGGCCAGGCTGGAG
 TGCAGTGGTGCATCTCAGCTCACTGCAACCCCGCCTCTGGTTCAAGCGATTCTCCTCC
 CCCAGCCTCCAAAGTGCTGGAGGACAGGTGTGAGCTGCCGCACCCAGCCTGTTCT
 TTCCACTCTCTTTCTCATCTCTTCTGGTTGCCCTGCGCTTATCTGCCTGT
 TTTGCAAGCACCTCTCTGTGTCCTGGAGCCCTGAGACTCTCTCTCCCT
 CCCACCTCCAAAGGTGCTGAGCTCACATCCACACCCCTGCAAGCCGTCCATGCCACAGCCCC
 CCAAGGGGCCATTGCCAAAGCATGCCCTGCCACCCCTCGCTGTGCCTAGTCAGTGTGTAC
 GTGTGTGTGTGTTGGGGGTGGGGGTGGTAGCTGGGATTGGCCCTCTTCT
 CCCAGTGGAGGAAGGTGTGCACTGTACTTCCCTTAAATTAAAAACATATATATAT
 ATTGGAGGTCAGTAATTCCAATGGCGGGAGGCATTAAGCACCACCCCTGGTCCCTAGG
 CCCGCCTGGCACTCAGCCTGCCAGAGATTGGCTCCAGAATTGGCCAGGCTACAGAACAC
 CCACTGCCTAGAGGCCATCTAAAGGAAGCAGGGCTGGATGCCTTACCCAACTATTCT
 CTGTGGTATGAAAAG

FIGURE 20

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727
<subunit 1 of 1, 322 aa, 1 stop
<MW: 35274, pI: 8.57, NX(S/T): 1
MPVTVRTTITTTSSSGLGSPMIVGSPRALTQPLGLLRLQLVSTCVAFSLVASVGAWTG
SMGNWSMFTWCFCFSVTLLIIILIVELCGLQARFPLSWRNFPITFACYAALFCLSASIIYPTTY
VQFLSHGRSRDHAIATFFSCIACVAYATEVAWTRARPGEITGYMATVPGLLKVLTFVACI
IFAFISDPNLYQHQPALEWCVAVYAICFILAAIAILLNLGECTNVLPPIPFPSSLGALLSV
LLYATALVILWPLYQFDEKYGGQPRRSRDVSCSRSHAYYCAWDRRLLAVAILTAINLLAYVAD
LVHSAHLVFVKV
```

Important features:

Transmembrane domains:

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192,
205-226, 235-255 and 294-312

N-glycosylation site.

amino acids 66-69

Glycosaminoglycan attachment site.

amino acids 18-21

FIGURE 21

GAACGTGCCACCATGCCAGCTAATTTGTATTAGTAGAGACGGGGTTTCAACATGTTGGCCAGGCAGCTGGTC
TTGAACCTCGTGCACCTCATGATCCGCTCACCTCGGCCCTCCAAAGTGCTGGGATTACAGGCATGAGCCACTGACGC
CTGGCCAGCCTATGCATTAAAGAAATTATTCTGTATTAGGTGCTGTCTAAACATTGGGCACTACAGTGACCA
AAACAGACTGAATCCCCAAGAGCCAAGACCAGTGAGGGAGACCAACAAGAAACAGGAAATGCAAAAGAGACCA
TTATTACTCACTATGACTAAGGGTCAAAATGGGTACGGTATGGAGAGTGATTGTTAAGAGACTACAGAGGG
AGGACAGACTACCAAGAGGGGGCCAGGAAAGCTCCTCTGACGAGGTGGTATTCAAGCCAAACTGGAAGAATGA
GAAAGAGCTAGCCAGCCTAGAATAGTCCAGAAGAGATGGGGGACTACACTCACTACACTTTGGCCTGAGAA
AATAGCATGGGATTGGAGGAGGCTGGGAAACACCACTTCTGCCGACCTGGCAGGAGGATTGAGGGCTTGAGA
AAGGGCAATGGCAGTAGCAGTAGAAAGGACAGGGTAGGAGCAGGGACTTGCAGGGTGAATCATTAGGTCTTATC
AACAGATATGGCAGCAAAGCCAGGGAGAATTGATGGTAATGCTGAGGTTGGAGCCAGGCTAGATGGGACAG
TGGTGGGTGATGCAAAGGAAAGAGGTAGGGAGCAGGGCCAGACGTGGGGAGAAGGTGTGGGGTTGGTTTCCA
TCTTGCCGAGTCTGCCGGAAATGTGGATGGGAAGACCAAGAGGGAGGAGCAAGGGCAGAGGGGAAGGGAATCTAA
AGAAGTCTGGATGCCACACTCTCTTCTCTCTCAGAGGTCTCACTCGTGGTCTTCAT
TTCCTGCCCTGCCTCCATCTCTCTGGGTGCTGGGAAAGTGAGGAGATTAGCTGAAGTTTGCTCTCGGGGCCTG
TCTGAATCTCATTGCTTCTGGGAGGACATAATTACCTGCTCTAGCTTATCATCTTACATTCCCTGTAG
CCACTGGGACATATGTGGTGTCTCCCTAGCTCTGTCTCCCTCATGCCTTGTGGTATGGGATGTTAG
GGGGAGGTCACTGCTGTCAGAGGGCAGTCACTTCTAATGGTGTACCAAGGGTAATGGGAGACACAGTC
GCGATGTCGCCAAGTCCGGCAGGCCCTAACTATCCAGGAGATCGTGCCTGGCAGGTCCTCCCTGCATGGT
ATGCAAGCCCTCCCA**ATG**TTCGGCCACTTGTCTTCTCCCTGGTACATCCCTTGGGAACACTGTTCT
GTGAGTACATGCTGGGTCTCCCTTCTCCCTGCTCAGGTGAATCTCAGGCCCTCTCCACCCAAAGGGTC
ACATGGATCCTAACACTCCACCCCTTCCACCTCCCTGACCTGTGCTCCCTGGCTGGTCTTACAGGCTTC
TCCACCCCTCCCTATCTCAGGTATTCCAGGTGGTGAAGGGACACGTGACCTACCCCTGGCTGGTCTTACAGGCTTC
GCCGAGTGGCTCACCTCATTGAGTGGAAAGGGCTGGAGCAAGCCAGTGACTCACCTGTCGCCCTGGAAATCAGCCT
TTTCTCTATTCAAGACCTCAGCGAGGGCAACAAGAGGCTCGTTGCAGCAGGAGTGGCTGAGCAGTTGCCA
TCGCGGAAGCCAAGCTCCGAGCATGGTCTCGGTGAGTGGCAGGACTCCACTGATGACTCCTATGAGGACT
TTGCTGGGGAATGGACACAGACATGGCTGGCAGCTGCCCTGGGCCACCTCAGGACCTGTCACCCGGC
ACCGGTTCTCCGGCTGTGCCAGGGCTCCGTGGAGCCTGAGAGCAGTGTACAGACCGTGTCCCCAGACA
CCCTGTGCTCTAGTCTGTGCAACCTGGAGGATGGGTGTGGCTCCCCGGCCGGTGGCTTCCAGCTGCTGG
GCGATGAGCTGCTCTGCCAAACTGCCAGCCGGAAAGTGCTTCCGAGCCTGGGCCACTGGAGGCC
AGGACTCACTACAACCTGCCCTCACAGAGTCTGCCCTTCCCCCGGGAGGAGGAGGCCAGCCCCCTGCAAGG
ACTGCCAGCCACTGCCACCACTAACGGGAGCTGGGAACGGCAGCGGCAAGCCTTGACCTGGCTTCTG
GGGTGGTGTCTTAGATGAGGATGAGGAGAGCCAGAGGAACAG**TGA**CCCCACATCATGCCCTGGCAGTGGCATGCA
TCCCCGGCTGTGCCAGGGCAGGCCCTGTGCCCAAGTGTTGGCTCAAGGCTCCAGCAGAGCTCCACAGCC
TAGAGGCTCCTGGAGCGCTCGCTTCTCCGGTGTGTTGCATGAAAGTGTGGAGAGGAGGCCAGGGCTG
GGCTGGGGCGCATGTCCTGCCCTCACTCCGGGCTTGCCGGGGCTGGCCGGGGCTCTGGGCATGGCTACA
GCTGTGGCAGACAGTGATGTTCATGTTCTAAATGCCACACACACATTCTCTCGGATAATGTGAACCACTA
AGGGGGTGTGACTGGCTGTGAGGGTGGGGTGGAGGGGCCAGCAACCCCCCACCTCCCATGCCCTC
TCTTCTGCTTTCTCATGCCAGTGCTGCCATGTGAGTGTGCTGATAGAATCACCCACCTGGAGGGCTGG
CTCCCTGCCCTCCGGAGCCTATGGGTGAGGCCCTCAAGGGGCCAGCTGGCTCGTGTGCTTC
ATTACACCTCTCATGTCCTAAATCTCTCTTTCTAAAGACAGAAGGGTTGGTCTGTTCTGTTTTCAGTC
GGATCTTCTCTCTGGGGAGGCTTGGGAATGATGAAAGCATGTAACCCCTCCACCTTCTGGCCCTAATGG
GGCCTGGGCCCTTCCCAACCCCTCTAGGATGTCGGGAGCTGTGCTGGCCCTCACAGCAGGCCGGCTGCC
ATTACGCCAGAGCTCTGAGCGGGAGGTGGAAGAAAGGATGGCTCTGGTGTGGCACAGAGCTGGACTTCATGTT
CTTCTAGAGAGGGCCACAAGAGGGCCACAGGGGTGGCGGGAGTTGTGAGCTGATGCCCTGTGAGAGGAGGAAT
TGTGCCAGTGAGTGACAGTCAGGGAGTGCTCTCTGGGGAGGAAGAAGGTAGAGCCTTCTGTCGAAT
GAAAGGCCAAGGCTACAGTACAGGCCCGCCCCAGCCAGGGTGTAAATGCCACAGTAGTGAGGCCCTGGCAG
ATCCTGCATTCCAAGGTCACTGGACTGTACGTTTATGGTTGTGGGAAGGGTGGCTTGAATTAAGG
CTTGTAGGCTTGGCAGGTAAGAGGGCCAAGGTAGAAACGAGGAGGCCAACGGGACAAGCATTCTATATAAGT
GGCTCATTAGGTGTTATTTGTTCTATTAAAGAATTGTTTATTAAATTAAATATAAAAATCTTGTAAATCTC
TAAAA

FIGURE 22

MFLATLSFLLPFAHPFGTVSCEYMLGSPLSSLAQVNLSFPSHPKVHMDPNYCHPSTSLHLC
LAWSFTRLLHPPPLSPGISQVVKDHVTKPTAMAQGRVAHLIEWKGWSKPSDSPALESAFSSY
SDLSEGEQELEARFAAGVAEQFAIAEAKLRAWSSVDGEDSTD SYDEDFAGGMDTDMAGQLPLG
PHLQDLFTGHRSRPRVQGSVEPESDCSQTVPDTLCSSLCSLEDGLLGSPARLASQLLGDE
LLLAKLPPSRESAFRSLGPLEAQDSLYNSPLTESCLSPAEEEPAPCKDCQPLCPPLTGSWER
QRQASDLASSGVVSLDEDEAEPEEQ

Signal peptide:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232,
285-289, 324-328

Tyrosine kinase phosphorylation site.

amino acids 44-52

N-myristoylation site.

amino acids 17-23, 26-32, 173-179

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 11-22

FIGURE 23

GGTCCTGGCGCTGTTACACAAGCAAGATAAGCCAGCCCCACCTAATTTGTTCCCT
 GGCACCCCTCCTGCTCAGTGCAGACATTGTACACTTAACCCATCTGTTCTCTAATGCACGA
 CAGATTCCCTTCAGACAGGACAACACTGTGATATTCAAGTTCAGTTCTGATTGAAATACCTCCTAAG
 CCTGAAGCTTCTGTTACTAGCCATTGTGAGCTCAGTTCTCATCTGCAAATGGCATAA
 TACAATCTATTCTGCCACATCAAGGGATTGTATTCTTAAAAAAACCAATACCAAAAG
 AAGCCTACA**ATG**TGGCCTAGCCAAAATTCTGTTGATTCAACGTTGTTTATTCACTTCT
 ATCGGGGAGCCATGGAAAAGAAAATCAAGACATAAACACACAGAACATTGCAGAAGTT
 TTAAAACAATGGAAAATAAACCTATTCTTGAAAGTGAAGCAAACCTAAACTCAGATAAA
 GAAAATATAACCACCTCAAATCTCAAGGCGAGTCATTCCCCTCCTTGAATCTACCCAAACAA
 CAGCCACCGAATAACAGATTCTCAGTAACTCATCAGCAGAGCATTCTGGCAGTCTAA
 AACCCACATCTACCATTCCACAAGCCCTCCCTGATCCATAGCTTGTCTAAAGTGCCT
 TGGAATGCACCTATAGCAGATGAAGATCTTGCCATCTCAGCACATCCAATGCTACACC
 TGCTCTGTCTCAGAAAACCTCACTGGTCTTGGTCAATGACACCGTAAAACCTCTGATA
 ACAGTTCCATTACAGTTAGCATCCTCTTCAGAACCAACTCTCCATCTGTGACCCCCCTG
 ATAGTGGAACCAAGTGGATGGCTTACCAACACAGTGTAGCTTCACTGGTTACCCCTTA
 TCAAGAAAAAAACAACCTACAGCCTACCTTAAAATTCAACAAATTCAAACACTTTCCAA
 ATACGTCAAGATCCCCAAAAGAAAATAGAAATACAGGAATAGTATTGGGGCATTAGGT
 GCTATTCTGGGTGTCATTGCTTACTCTGTGGCTACTTGTGTGGAAAAAGGAAAAC
 GGATTCAATTCCCCTCGCGACTTTATGACGACAGAAATGAACCAAGTTCTGCGATTAGACA
 ATGCACCGAACCTTATGATGTGAGTTGGATTCTAGCTACTACAATCCAACCTTGAAT
 GATTCAAGCCATGCCAGAAAGTGAAGAAAATGACGTGATGGCATTCTATGGATGACATACC
 TCCACTTCGTACTTCTGTA**TAGA**ACTAACAGCAAAAGGCGTTAACAGCAAGTGTCACTA
 CATCCTAGCCTTTGACAAATTCACTTTCAAAAGGTACACAAAATTACTGTCACGTGGAT
 TTTGTCAAGGAGAATCATAAAAGCAGGAGACCAGTAGCAGAAATGTAGACAGGATGTATCAT
 CCAAAGGTTTCTTCTTACAATTGGCATCCTGAGGCATTACTAAGTAGCCTTAATT
 TGTATTTAGTAGTATTCTTAGTAGAAAATTTGTGGATCAGATAAAACTAAAGATT
 TCACCATTACAGCCCTGCCTCATAACTAAATAAAAAATTATTCCACCAAAAAATTCTAAA
 ACAATGAAGATGACTCTTACTGCTCTGCCTGAAGCCCTAGTACCAATTCAAGATTGCAT
 TTTCTTAAATGAAAATTGAAAGGGTGTGTTAAAGAAAATTGACTTAAAGCTAAAAGAG
 GACATAGCCCAGAGTTCTGTTATTGGGAAATTGAGGCAATAGAAAATGACAGACCTGTATT
 TAGTACGTTATAATTCTAGATCAGCACACACATGATCAGCCACTGAGTTATGAAGCTGA
 CAATGACTGCATTCAACGGGCCATGGCAGGAAAGCTGACCCCTACCCAGGAAAGTAATAGCT
 TCTTAAAGTCTCAAAGGTTTGGGATTAACTTGTCTTAATATATCTTAGGCTTCAA
 TTATTTGGGTGCCTAAAAACTCAATGAGAATCATGGT

FIGURE 24

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732
><subunit 1 of 1, 334 aa, 1 stop
><MW: 36294, pI: 4.98, NX(S/T): 13
MLALAKILLISTLFYSLLSGSHGKENQDINTTQNIAEVFKTMENKPISLESEANLNSDKENI
TTSNLKASHSPPLNLPNNSHGITDFSSNSSAEHSLGSLKPTSTISTSPPPLIHSFVSKVPWNA
PIADEDLLPISAHPNATPALSSENFTWSLVNDTVKTPDNSSITVSILSSEPTSPSVTPLIVE
PSGWLTTSNDSFTGFTPYQEKTTLQPTLKFTNNSKLFPNTSDPQKENRNTGIVFGAILGAIL
GVSLLTLVGYLLCGKRKTDSFSHRRLYDDRNEPVLRLDNAPEPYDVSFGNSSYYNPTLNSA
MPESEENARDGIPMDDIPPLRTSV
```

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 235-262

N-glycosylation site.

amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159,
163-167, 218-222, 225-229, 298-302, 307-311

FIGURE 25

AACAGGATCTCCTTGCAGTCTGCAGCCCAGGACGCTGATTCCAGCAGCGCCTTACCGCGC
 AGCCCGAAGATTCACT**ATGGT**GAAAATCGCCTCAATAACCCCTACGCCGTGAAAAGGAGG
 AGGCGCGGAAGACGTGGAGGCCCTCCTGAGCCGACGGTCAGAACTCAGATACTGACCGGC
 AAGGAGCTCGAGTGCACCCAGGAAAAGAGGGCTCCTCTGGGAGATGTATGCTTACTCT
 CTTAGGCCTTCATTCATCTTGGCAGGACTTATTGTTGGAGGCCTGCATTACAAGTACT
 TCATGCCAAGAGCACCATTACCGTGGAGAGATGTGCTTTTGATTCTGAGGATCCTGCA
 AATTCCCTCGTGGAGGAGAGCCTAACCTCCTGCCTGTGACTGAGGAGGCTGACATTGTGA
 GGATGACAACATTGCAATCATTGATGTGCCTGCCCCAGTTCTGTGATAGTGACCCCTGCA
 CAATTATTCATGACTTGAAAAGGAATGACTGCTTACCTGGACTTGTGCTGGGAACTGC
 TATCTGATGCCCTCAATACTTCTATTGTTATGCCTCCAAAAATCTGGTAGAGCTCTTGG
 CAAACTGGCGAGTGGCAGATATCTGCCTCAAACCTATGTGGTCGAGAAGACCTAGTTGCTG
 TGGAGGAAATTGATGTTAGTAACCTGGCATCTTACCAACTTGCAATAACAGA
 AAGTCCTCCGCCTCGCAGAGACCTCTGCTGGTTCAACAAACGTGCCATTGATAA
 ATGCTGGAAGATTAGACACTCCCCAACGAATTATTGTTGAGACCAAGATCTGTCAAGAG**T**
AAGAGGCAACAGATAGAGTGCCTGGTAATAAGAAGTCAGAGATTACAATATGACTTAA
 CATTAAGGTTATGGGATACTCAAGATATTACTCATGCATTACTCTATTGCTTATGCTTT
 AAAAAAAGGAAAAAAAAAAACTACTAACCAACTGCAAGCTTGTCAAATTAGTTAAT
 TGGCATTGCTGTTTTGAAACTGAAATTACATGAGTTCATTTCCTTGCAATTAG
 GGTTAGATTCTGAAAGCAGCATGAATATATCACCTAACATCCTGACAATAAATTCCATCC
 GTTGTGTTTTGTTGTTGTTCTTCTTAAGTAAGCTTTATTGATCTTATG
 GTGGAGCAATTAAAATTGAAATATTAAATTGTTGAACCTTTGTGAAATATA
 TCAGATCTCAACATTGTTGGTTCTTGTGTTCTTGTACAACTTCTGAAATTAGA
 AATTACATCTTGCAGTTCTGTTAGGTGCTCTGTAATTAAACCTGACTTATATGTGAACAATT
 TTCATGAGACAGTCATTAACTAATGCAGTGATTCTTCTCACTACTATCTGATTGTGG
 AATGCACAAAATTGTGTAGGTGCTGAATGCTGTAAGGAGTTAGGTGTATGAATTCTACAA
 CCCTATAATAAATTACTCTACAAAAA

FIGURE 26

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828
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ILAGLIVGGACIYKYFMPKSTIYRGEMCFFDSEDPANSLRGGEPNFLPVTEEADIREDDNIA
IIDVPVPSFSDPAAIIHDFEKGMTAYLDLLLGNCLMPLNTSIVMPPKNLVELFGKLASG
RYLPQTYVVREDLVAVEEIRDVSNLGIFIYQLCNNRKSFRRLRRDLLLGFNKRAIDKCWKIR
HFPNEFIVETKICQE
```

Type II transmembrane domain:

amino acids 53-75

N-glycosylation site.

amino acids 166-170

Casein kinase II phosphorylation site.

amino acids 35-39, 132-136, 134-138

N-myristoylation site.

amino acids 66-72, 103-109

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 63-74

FIGURE 27

GGAGGAGGGAGGGCGGGCAGGCCAGCCCAGAGCAGCCCCGGCACCGACGGACTCTCT
 CTTCCAGCCCAGGTGCCCTTCACTCTCGCTCCATTGGCGGGAGCACCCAGTCCTGTACGCC
 AAGGAACCTGGTCTGGGGCACC**ATG**TTTCGGCGGCAGCCCCAGCCTCCTCATCCTTCTG
 TTGCTGCTGCTGGGGTCTGTGCCTGCTACCGACGCCGCTCTGTGCCCTGAAGGCCACGTT
 CCTGGAGGATGTGGCGGGTAGTGGGGAGGCCAGGGCTCGTCGGCCTCCTCCCCGAGCCTCC
 CGCCACCCTGGACCCGGCCCTCAGCCCCACATCGATGGGCCAGCCCACAACCCCTGGGG
 GCCCATCACCCCCCACCACCTCCTGGATGGGATAGTGGACTTCTCCGCCAGTACGTGAT
 GCTGATTGCTGTGGTGGGCTCCCTGGCCTTCTGCTGATGTTATCGTCTGTGCCCGGTCA
 TCACCCGGCAGAACGAGAACGGCCTCGGCCTATTACCCATCGTCCTCCCCAAGAACAGTAC
 GTGGACCAGAGTGACCGGGCGGGGGCCCCGGGCTTCAGTGAGGTCCCCGACAGAGCCCC
 CGACAGCAGGCCCGAGGAAGCCCTGGATTCCCTCCGGCAGCTCCAGGCCACATTTGGCCG
 CCACCCAGAACCTCAAGTCCCCCACCAGGGCTGCACTGGCGGTGGGACGGAGCCAGGATG
 GTGGAGGGCAGGGCGCAGAGGAAGAGGAGAACGGCAGCCAGGAGGGGACCAAGGAAGTCCA
 GGGACATGGGTCCCAGTGGAGACACCAAGGGCGCAGGAGGAGCCGTGCTCAGGGTCCTTG
 AGGGGGCTGTGGTGGCGGTGAGGGCCAAGGGGAGCTGGAAGGGTCTCTCTGTTAGCCAG
 GAAGCCCAGGGACCAGTGGTCCCCCGAAAGCCCTGTGCTGCAGCAGTGTCCACCCAG
TGTCTAACAGTCCTCCGGCTGCCAGCCCTGACTGTCGGCCCCAAGTGGTACCTCCCC
 GTGTATGAAAAGGCCCTCAGCCCTGACTGCTTCCTGACACTCCCTCCTGGCCTCCCTGTGG
 TGCCAATCCCAGCATGTGCTGATTCTACAGCAGGCAGAAATGCTGGTCCCCGGTCCCCGG
 GGAATCTTACCAAGTGCATCATCCTCACCTCAGCAGCCCCAAAGGGTACATCCTACAGC
 ACAGCTCCCCGACAAAGTGAGGGAGGGCACGTGTCCCTGTGACAGCCAGGATAAAACATCC
 CCCAAAGTGTGGATTACAGGCAGGCGTGCAGGCCACCGTGCCTGGCCCAAACACTACTTTAAAACA
 GCTACAGGGTAAAATCCTGCAGCACCCACTCTGGAAAATACTGCTCTTAATTTCTGAAGG
 TGGCCCCCTGTTCTAGTTGGTCCAGGATTAGGGATGTGGGTATAGGGATTAAATCCTC
 TCAAGCGCTCTCCAAGCACCCCCGGCTGGGGTGAGTTCTCATCCGCTACTGCTGCTGG
 GATCAGGTTGAATGAATGGAACCTTCCTGTCTGGCCTCCAAAGCAGCCTAGAAGCTGAGGG
 GCTGTGTTGAGGGACCTCCACCTGGGAAGTCCGAGGGCTGGGAAGGGTTCTGACG
 CCCAGCCTGGAGCAGGGGGCCCTGGCACCCTGTTGCTCACACATTGCTGGCAGCCTG
 TGTCCACAATATTGTCAGTCCTCGACAGGGAGCCTGGCTCCGTGCTTCTGAGGAGGCT
 CTGGCAGGAGGTCTCTCCCCATCCCTCCATCTGGGCTCCCCAACCTCTGCACAGCTCT
 CCAGGTGCTGAGATATAATGCACCAAGCACAATAAACCTTATTCCGGCCTGAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGA

FIGURE 28

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852
><subunit 1 of 1, 283 aa, 1 stop
><MW: 29191, pI: 4.52, NX(S/T): 0
MVSAAAPSILLLLLLLGSVPATDARSVPLKATFLEDVAGSGEAEGSSASSPSLPPPWTPAL
SPTSMGPQPTTLGGPSPPTNFLDGIVDFFRQYVMLIAVVGSLAFLLMFIVCAAVITRQKQKA
SAYYPSSFPKKKYVDQSDRAGGPRAFSEVPDRAPDSRPEEALDSSRQLQADILAATQNLKSP
TRAALGGGDGARMVEGRGAEEEKGSQEGDQEVTQGHGVVPETPEAQEEPCSGVLEGAVVAGE
GQGELEGSLLLQAQEAQGPVGPPESPCACSSVHPSV
```

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 94-118

N-myristoylation site.

amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199,
211-217, 238-244, 242-248

FIGURE 29

FIGURE 30

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212
 ><subunit 1 of 1, 440 aa, 1 stop
 ><MW: 42208, pI: 6.36, NX(S/T): 1
 MKFQGPLACLLLALCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGA
 AGSKVSEALGQGTREAVGTGVRQVPGFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHG
 ADAVRGWSQGVPGHSGAWETSGGHGIFGSQGGLGGQGQGNPGGLGTPWVHGYPGNSAGSFGM
 NPQGAPWGQGGNGGPPNFGTNTQGAVAQPGYGSVRASNQNEGCTNPPPSGGSSNSGGGS
 GSQSGSSGSGSNGDNNNGSSSGSSSGSSGGSSGGSSGNSGGSRGDGSESSW
 GSSTGSSSGNHGGSGGGNGHPGCEKPGNEARGSGESGIQGFRQGVSSNMREISKEGNRLL
 GGSGDNYRGQGSSWGSGGDAVGGVNTVNSETSPGMNFDTFWKNFKSKLGFINWDAINKDQ
 RSSRIP

Signal peptide:

amino acids 1-21

N-glycosylation site.

amino acids 265-269

Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70, 74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158, 155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205, 218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252, 249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281, 279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298, 295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328, 323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387, 383-389, 387-393, 389-395, 395-401

Cell attachment sequence.

amino acids 301-304

FIGURE 31

GACCGGGCTCCCTCCGGTCTGGATGTGCGGACTCTGCTGCAGCGAGGGCTGCAGGCCGCCGGCGGTGCTCACCG
TGCCCTGGCTGGGGAGTTCTCCTTGCACCATGTTGTCCTGCTGGAATATTACCGGGACATCTTCA
CTCTCCTGCTGCCCTGCACCGGAGCTGGTGTGCGAGGAGAGTGGAGGGAAAGATGTTCTCTGAACAAGC
TGCTGCTACTTGCTGCTGGCTGGCTTTCCAGATTCCCACAGTCCCTGAGGACTTGTCTTCTGGAAAGAGG
GTCCTCATATGCCCTTGAGGTGGACACAGTAGCCCCAGAGCATGGCTGGACAATGCGCCTGTTGGACCAGC
AGCTGCTCTACACCTGCTGCCCTACATCGGAGAGCTCCGGAAACTGCTGCTCGCTGTTGGTGTAGGCAGTAGTG
GACGGAGTGGGGCTCATGAGGAAAATCACCCCCACCACTACCACCGAGCTGGGAGGCCAGCCTCCAGACCA
GCCAGGGCTGCAGGCACAGCTGCCAGGCCTTTCCACAAACAGGCCCTCCTGCGCCGACCGTAGAGT
TCGTGGCAGAAAGAATTGGATCAAACATGTGTCAAACATATCAAGGCTACACTGGTGGCAGATCTGGTGCGCCAGG
CAGAGTCACCTCTCAAGAGCAGCTGGTGCACACAGGGAGAGGAAGGGGAGACCCAGCCCAGCTGTTGGAGATCT
TGTGTTCCAGCTGTGCCCTACGGGGCCCAGGCATTGGCCCTGGGCGGGAGTTCTGTCAAAGGAAGAGCCCTG
GGGCTGTGCCGGCCTGCTCCAGAGGAGACCCGGCAGCCGTTCTGAGCAGTGCAAGAGAACATTGCTGTTGGG
TTGCAACAGAGAAAGCCTGTGCTTGCTGCAAGAACATCACGACTGATCAGGAGGGAGGTGAAAGCAGCAG
TGAGTCGCACACTTCGAGGCCAGGGTCTGAAACCTGCTGCCCGGGGGAGCGGGAGGGCTGCTCCCGCGCT**TGA**
GTGCTCTCCTTGGCGTGGGCCACGGGACCTGACGAGGGAGTCTCCCAGAGCATCTGGAACAGCTCTTAGGC
CAGCTGGGCCAGACGCTGCGGTGCCAGTCCCTGTGCCACCTGCTGAGCAGCATCTGGCAAAAGTGTCTGTG
GAGTTAGCTTCCCTCCTGTCAGATCAAATTCTATCCTAGGGCCCCCGGCACAGTACAGGCTGGAGAGAGGG
CAGGCTCGAAGGCTCTGCACATGCTGCTTCTTGTGGAAGGAAGACTTCAGGGGCCGTTCCGCTGAGCTG
CTGCTGAGCCAAGAAATGTGGGGCTCTGGCAGACACAAGGCCAAGGGAGTGGGACTTGTCTGATTCTGCTA
CGGGAGCTGGTGGAGAAGGGCTGATGGGACGGTGGAGATAGAGGCTGCCCTGGCAGCCTCACCAGGGCCAG
TGGCAGGGGACTTGTGTAAGAAATTAGCAACACTGTCTAATCTGTTCTAGCCGAGCCCCACTGCCAGAACCC
CAGCTAAGAGCCTGTGAGTTGGTGCAGCCAAACCGGGCACTGTGCTGGCCAGAGCTAGGGCTGAGAAGTGGCC
CTGCCCTGGCATTGCAACAGAACCTGGACCCCGCCTCACAGGAGGGCCAAGTGCCCAATGCAAGACCTC
TGGTTGGGTGTAAGCTGGCTACAGTCAGACTCCCTGCTTAAGGGTGTCACTGCTGGCATCCCACACCGCA
ATCCTAGAGGAAGGAGAGTGGCTGATTTGGATTATGGCAAAAAGTCCAGAGATGCCAGTCTGGAGTAGAA
GAGGTGGTGTGTTATCTCTGGATACTAAATGAAATGAGGTGTGTTGCAACACAGAATTCAAGCCT
CATTTGCTATCCCAGCATCTCTAAACCTTGAGTCTGGAAATTCTGACAGAGGCAAAATGACTCTGCTTAAC
TTATGAAGAAAGTTAAACATGAATCTGGGAGTCTACATTCTTATCACAGGAGCTGGACTGCCATCTC
ATAAAATGCCAACACAGGGCTGCTGGTGGCTCATGCCGTAAATCCCAGCACTTGAGAGGCCGAGGGTGGC
GACTGCCCTGAGGTCAAGACAGCCTGGCAACATGGCAAAACCCCCATCTACTAAAAA
TTATTAGCTGGCATGGTGGTGTGCCCTGTAATCCCAGCTACTCAGGAGGATGAGGAGACCTGCTGAAC
CTGGAGGTGGAGGTGCAGTGAGCCGAGGTGCACTGCCAGTCTGGTAACAGAGCAGACTTCTAG
AAAAAGCTAACAAACAGATAAGGTAGGACTCAACCAACTGAAACCTGACTTCCCTGTAACCTGCCCTG
TGCAGGTAGTAACCTCTGAGACCTCTCCCTGACCAAGGGACCAAGCACAGGGCATTAGAGCTTTAGAATAAA
CTGGTTTCTTAAAGGGCTTTTATTAAAGGGCTTTTATTAAATCTCCCACAGCATGGCTCTGCAACAGCTC
TTTTTTTTTTTTTTTTAAAGGGCTTTTATTAAATCTCCCACAGCATGGCTCTGCAACAGCTC
TGGGGCGCTGCTGTAGGGAAAGGCCCTGTTCTGGCTGAGGCGGGGCTGGCTGTCATGGTCCGGAGCTG
GCCGCTGCTGGCGGCTGGCGCTGTAGCTGCTCTTGGCGGACAGAGCTGGGGCTGGGGGCC
AGCTAACAGAGCAGGGCTGGTGTAGGGTGTGGGGACTCATGGGAATGCCCTGAGGAGCTACGTG
GGTCCACCTGAGTGGCACGGGAGCAGCTGTGGCGGCTGCTCTTCYTAGGCCAGCTGGGAAACTAACAGCTC
GGGCCCTCTTGCAAAAGACCGAGGATGGGTGTGGGGACTCATGGGAATGCCCTGAGGAGCTACGTG
GAAGAGGGCGCCGTTTGTGGCTGAGCGGCCCTGGAGCGCTCTCTGAGCCTCAGTTCCCTTCCGCTCA
ATGAAGAACATGCCGCTCGGTGTCAGGGCTATTAGGACTTGCCCTCAGGAAGTGGCCTTGACGAGCGTCA
GTTATTTACAACATGTCTGCGACGTTGGCTGGCACGTATGGAATGGCCCATGTCCTCTGCTGCGTGGAC
GTCGCGGTGGAGGTGCGCAGCCAGAGGGGGCAGACGTGCGCTGGGGTGAGGGAGGGGCCGGGG
CCTCACAGGAAGTGGCTCCGCACCAACAGGCAGGGCGGCTCCGCCGCCGCCACACCAGTCCAGG
GGCGGTAGACAAAGTGGAGTCGCGCTGGCTCGCTGCGCAGCAGGTAGCCCTGATGCACTGCGCAGCGC
TGTGTCGCCAGCTGGAAGCAGCGCCCGTCCACAGCACGAACAGCCGGTGC
GCT

FIGURE 32

MCFLNKLLLLAVLGWLFOIPTVPEDLFFLEEGPSYAFEVDTVAPEHGLDNAPVVDQQLLYTC
CPYIGELRKLLASWVGSSGRSGGFMRKITPTTTSLGAQPSQTSQLQALAQAFFHNQPP
SLRRTVEFVAERIGSNCVKHIKATLADLVRQAESLLQEQLVTQGEEGGDPAQLLEILCSQL
CPHGAQALALGREFCQRKSPGAVRALLPEETPAAVLSSAENIAVGLATEKACAWLSANITAL
IRREVKAAVSRTLRAQGPEPAARGERRGCSRA

Signal peptide:

amino acids 1-18

N-glycosylation site.

amino acids 244-248

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 89-93

Casein kinase II phosphorylation site.

amino acids 21-25, 167-171, 223-227

N-myristoylation site.

amino acids 100-106, 172-178, 207-213

Microbodies C-terminal targeting signal.

amino acids 278-282

FIGURE 33

TCCCTTGACAGGTCTGGTGGCTGGTCGGGCTACTGAAGGCTGTCTGATCAGGAACTG
 AAGACTCTGCTTTGCCACAGCAGTCAGCTGCAGCTCAGGAGGTGTGAACCCACATCCC
 TGCCCCCAGGGCACCTGCAGGACGCGACACCTACCCCTCAGCAGACGCCGGAGAGAA**ATG**
 AGTAGCAACAAAGAGCAGCGTCAGCAGTGGTGTGATCCTCTTGCCTCATCACCACCT
 CATCCTCTACAGCTCAACAGTGCATGAGGTCTTCCATTACGGCTCCCTGCAGGGCGTA
 GCCGCCGACCTGTCAACCTCAAGAAGTGGAGCATCACTGACGGCTATGTCCCATTCTCGGC
 AACAAAGACACTGCCCTCTCGTGCACCACTGAGTGTGATTGTGACAGCAGCTCCAGCCACCTGCT
 GGGCACCAAGCTGGCCCTGAGATCGAGCGGGCTGAGTGTACAATCCGCATGAATGATGCAC
 CCACCACTGGCTACTCAGCTGATGTGGCAACAAGACCACTACCGCGTGTGGCCCATTCC
 AGTGTGTTCCCGCGTGTGAGGGAGGCCCCAGGAGTTGTCAACCGGACCCCTGAAACCGTGT
 CATCTCTGGGGGCCCGAGCAAGATGCAGAACGCCCCAGGGCAGCCTCGTGTGATCC
 AGCGAGCGGGCTGGTGTCCACATGGAAAGCATATGCCGTCTCTCCGGCCGCATGC GG
 CAATTGACGACCTCTCGGGGTGAGACGGCAAGGACAGGGAGAAGTCTCATTGTGGTT
 GAGCACAGGCTGGTTACCATGGTGTGCGGGTGGAGTTGTGACCATGTCATGTCTATG
 GCATGGTCCCCCCTACTACTGCAGCCAGCGGGCCCGCCTCCAGCGCATGCCCTACCAACTAC
 TACGAGCCCAAGGGGCCGGACGAATGTGTCACCTACATCCAGAATGAGCACAGTCGCAAGGG
 CAACCAACCACCGCTTCATCACCGAGAAAAGGGCTTCTCATCGTGGGGCCAGCTGTATGGCA
 TCACCTCTCCCACCCCTCTGGACCT**TAG**GCCACCCAGCCTGTGGACCTCAGGAGGGTCAG
 AGGAGAACGAGCCTCCGCCAGCGCTAGGCCAGGGACCATCTCTGGCCAATCAAGGCTTG
 CTGGAGTGTCTCCAGCCAATCAGGGCTTGAGGAGGATGTATCTCCAGCCAATCAGGGCC
 TGGGAATCTGTTGGCGAATCAGGGATTGGAGTCTATGTGGTTAATCAGGGGTGTCTTTC
 TTGTGCAGTCAGGGCTGCGCACAGTCAATCAGGGTAGAGGGGGTATTCGAGTCAATCTG
 AGGCTAAGGACATGTCCCTTCCATGAGGCCTGGTTCAGAGCCCCAGGAATGGACCCCCCA
 ATCACTCCCCACTCTGCTGGATAATGGGGCTGTCCAAAGGAGCTGGAACTTGGTGTG
 CCCCTCAATTCCAGCACCAGAAAGAGAGATTGTGTTGGGGTAGAAGCTGTCTGGAGGCC
 GGCCAGAGAATTGTTGGGGTTGTGGAGGTTGTGGGGGGCGGTGGGAGGTCCCAGAGGTGGGA
 GGCTGGCATCCAGGTCTGGCTCTGCCCTGAGACCTTGACAAACCCCTCCCTCTGG
 CACCCCTCTGCCACACCAGTTCCAGTGCAGGAGTCTGAGACCCCTTCCACCTCCCTACAA
 GTGCCCTCGGGCTGTCCTCCCCGTGGACCCCTCCAGCCACTATCCCTGCTGGAAAGGCT
 CAGCTCTTGGGGGTCTGGGTGACCTCCCCACCTCTGGAAAACCTTGTAGGGTATTTTGC
 GCAAACCTTCAGGGTTGGGGACTCTGAAGGAAACGGGACAAACCTTAAGCTGTTTCT
 TAGCCCCCTAGCCAGCTGCCATTAGCTGGCTCTTAAAGGGCCAGGCCTCTTCTGCCCT
 CTAGCAGGGAGGTTTCCAACCTGTTGGAGGCGCTTGGGGCTGCCCTTGTCTGGAGTCA
 CTGGGGCTTCCGAGGGCTCCCTGACCCCTCTGTCGTCTGGATGGCTGTGGAGCTGT
 ATCACCTGGGTCTGCCCCTGGCTCTGTATCAGGCACCTTATTAAAGCTGGGCCTCAGTGG
 GGTGTGTTGTCTCTGCTCTGGAGCCTGGAAGGAAAGGGCTTCAGGAGGAGGCTGTGA
 GGCTGGAGGGACCACTGGAGGAGGCCAGCAGCTAGCCATTGCACACTGGGGTGTGGGG
 GGGCGGTGACTGCCCAAGACTTGGTTGTAATGATTGTACAGGAATAAACACACACCTACGC
 TCCGGAAAAA

FIGURE 34

MSSNKEQRSAVFVILFALITILYLSSNSANEVFHYGSLRGRSRRPVNLKKWSITDGYVPIL
GNKTLPSRCHQCVIVSSSSHLLGTKLGPEIERAECTIRMNDAPTTGYSAVGNKTTYRVVAH
SSVFRVLRRPQEFVNRTPETVFIFWGPPSKMQPQGSLVRVIQRAGLVFPNMEAYAVSPGRM
RQFDDLFRGETGKDREKSHSWLSTGWFTMVIACHELCDHVHVVGMVPPNYCSQRPRQLQRMPYH
YYEPKGDECVTYIQNEHSRKGNHHRFITEKRVFSSWAQLYGITFSHPSWT

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 9-31 (type II)

N-glycosylation site.

amino acids 64-68, 115-119

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 50-54

Casein kinase II phosphorylation site.

amino acids 3-7, 29-33, 53-57, 197-201

Tyrosine kinase phosphorylation site.

amino acids 253-262

N-myristoylation site.

amino acids 37-43, 114-120, 290-294

FIGURE 35

GTTTCTCATAGTTGGCGTCTTCTAAAGGAAAAACACTAAAATGAGGAACCTAGCGGACCAGGGAGCGACGCAGCTT
 GAGGGAAAGCATCCCTAGCTGTGGCGCAGAGGGCGAGGGCTGAAGCCGAGTGGCCCGAGGTGTCTGAGGGGCTGG
 GGCAAAGGTGAAAGAGTTTCAAGAACAAAGCTTCTGGAAACCATGACCCATGAAGTCTTGTGACACATTATAACCGT
 CTGAGGGTAGCAGCTGAAACTAGAAGAAGTGGAGTGTGAGGACGGCAGTATCTCTTGTGTGACCCCTGG
 GGCTATGGGACGTTGGCTCAGACCTTGTGATACACCAT**G**CTGCGTGGGACGATGACGGCGTGGAGAGGAATG
 AGGCCTGAGGTACACTGGCTTGCCCTCTCCTAGCCACAGCAGGCTGCTTGTGACTTGATCTGGGCTGCGTGGTGA
 GACCGTCCAGCCTGCGTCCACCGTCCAGAAGCCGGAGGCAGTGTGATCTGGGCTGCGTGGTGA
 AGGATGAATGTAACCTGGCGCTGAATGGAAGGAGCTGAATGGCTCGGATGATGCTCTGGGTGTCCTCATCACC
 CACGGGACCCCTCGTCATCACTGCCCTTAACAACCACACTGTGGGACGGTACCAAGTGTGCCCCGGATGCCTGCG
 GGGGCTGTGGGCCAGCGTGCACGCCACTGTGACACTAGCCAACTCCTCAGGACTCTCAAGTTAGATGTGACCGT
 ATTAAGTGGATGAGGGAAACACAGCAGTCACTGGCTGCCACCTGCGTGGAGGCCACCCCAAAGGCCAGGTC
 TACAGCGTCAAACAAGAGTGGCTGGAGGCCAGAGGTAACCTACCTGATCATGCCCTCAGGGAACCTCCAGATT
 GTGAATGCCAGGCCAGGAGGACAGGGCATGTACAAGTGTGAGCCTACAACCCAGTGACCCAGGAAGTGA
 AACCCCTCCAGCGACAGGCTACGTGTGCCGCTCCACCGCTGAGGCTGCCGATCATCTACCCCCCAGAGGCC
 CAAACCATCATCGTCACCAAAGGCCAGAGTCTCATTCTGGAGTGTGAGGCCAGTGGAAATCCCACCCCCAGGGC
 ACCTGGGCCAGGATGGTCCAGTGTACCGCTACAACAAAGACGCCCTCTGCTGAGCAACCTCCATCGAC
 ACCACCGAGG
 ATCTCTCATACATGTCAGGTGTTGAACCCCTGAGGTACCATGGAGCTATCCAGCTGCTGTCATCCCCGG
 CAGAGTGCAGCTACCTGTGAGGTGCGTGGAAACCCCCCGCCCTCGCTGCTGAGGAATGCTGTGCC
 CTCATCTCCAGGCCAGGCCCTCCGGCTCTCCCGCAGGGCCTGCGCTGCTCAGCATGGGGCCTGAGGAGC
 GTCTACCAGTGCATGCCAGAGGAGGTTGGAGGCCATGCCGTAGTCCAGCTGCCGACCTCCAGGCCAAC
 ATAACCCAAGGCTATGGCAGGATGCTGAGCTGGCTACTGGCACACCTCTGTATCACCTCCAAACTCGGCAAC
 CCTGAGCAGATGCTGAGGGGCAACCGCGCTCCCCAGACCCCCAACGTCAGTGGGCGCTGCTTCCCGAAGTGT
 CCAGGAGAGAAGGGCAGGGGCTCCCGCAGGGCTCCCGCAGGGCCTGCTGAGGAGCAGGCCACCTCAAGACAG
 TCATATGAACTGGTGTGGGGCTCCGGCTGAGGGCAGTGGCCGGGCCAACCTCTACTATGTGGTAAACAC
 CGCAAGCAGGTACAAATTCTCTGACGATTGGACCATCTCTGGCATTCCAGCAGCACCGCCCTGACCTC
 ACCAGACTTGACCCGGAGCTTGTATGAAGTGGAGATGCCAGCTACAACCTGTGCGGGAGAGGGCAGACAGC
 ATGGTCACCTTCCGAACTGGACGGGCCAACCCGAGATCATGCCAGCAAGAGCAGCAGATCCAGAGAGAC
 GACCCCTGGAGGCCAGTCCCCAGAGCAGCCAGGCCAGACCCGGCCCTCTCCCCCCCAGAAGCTCCGACAG
 CCCACCATCTCCAGGCCCTCCGGCTGAGGACCTCAGTGTACGTGACCTGGATTCCCGTGGGAATGGTGG
 CACATCAGTCTCCGGCTGAGGAGACTGGATTCTGGCACCAGGCCATCCCCCA
 TCGGGCTGTCCGTGGAGATCACGGGCCACTAGAGAAAGCACCCTCTAACAGTTCTGAGTCGGGCTCTGA
 ACATGCTGGGGAGAGCGAGGCCAGCGCCCCCTCTGGCCCTACGTGGTGTGGCTACAGCGGTGCGGT
 CAGAGG
 CCAGCAAGTAACAACAACACCCCAATCCATGCCCTTATATCTATTATGACCCACAGACAGTGA
 CAATGATGATGACTGACAAAGAAGCTAAAGAAAGTGGAGACTGGATTCTGGCACCAGGCCATCCCCCA
 GACTACAAGAAGGATATGGTGGAAAGGGGACAAGTACTGGCACTCCATGCCACCTGAGGCCAGAGAC
 GACATTAAGATGCACTGCTTCAATGAAAGGAGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG
 CGGAAGTCTCTGGCCAGCTGGTCACTGCCACCCCCAACCTCTGGGCCCCACAGGCCGCCCCCT
 ATAGAGCGGGCGGTGGGACTGGGCCATGGTGGCTCGCTCAGCGACCTGCCCTATCTGATTGT
 CGGGCTCCATCGTCTCATCGTCACCTCATCCCCCTCTGCTGTGGAGGGCTGGCTAAGCA
 ACAACAGACCTGGTTTCCTCGAAGTGCCCTCACCCCTCTGCCGTATAACTATGGTGC
 CCAGGCCACCCAGGCCAGTGGACAGGCCCTACCTCAGTGGCATCAGTGGACGGGCTGTG
 CTAAATGGGATCCACATG
 AATAGGGCTGCCCTCGGTGCACTGGCTACCCGGCATGAAGGCCAGCAGCACTGCCAG
 CAGCAGAGTGAACCCAGCAGCCCTGAGGAGGCCATCTGGCAATGGATATGCC
 ACAGGGGGTCCAAGTCTAGCCGGACGGGCTTCTTCTTATACACACTGCC
 CAGACTGCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
 CCGACAGTCTGTCTGGAAAGCAGTGTGGACCCCTCCATTCACT
 CAGGGCCCCCATGCTGCTGGGCTGGCTGGGCT
 CCAGTGTGAGAGGTGGACAGTCTGTGACTCTGCCAAGTGTGAGTGGAG
 GAGACTGGTGTCCCAGCAGGCCAG
 GCCTACGTAGGACAGGAACCTGGAAATGCA
 GACTCTCCCCGGGGCCACTGGTGC
 GTGTCTTTGAAACACCACCT
 CTACAAATT**TAG**CGAGAAGCTGATATCCCAGAAGAAGACTATATGTT
 TTT
 AGAGACAGAGAAAAATTGGTATTATTTCTTATATAGCCATATTATATTT
 TATGACTGTGAAATAATGTA
 TATGTTTATAATTCTGGAGAGACATAAGGAGCCTACCCGTTGAGGT
 TGAGGGAAACAGGAAACAGCAGGCCACAGGCTGGCGGGACAGACT
 CCTAACAGGAGTCACCCAGGAAAGCAGGCCACAGGCTGGCGGG
 ACAGACTCTAACCTGGGCTCTGCA
 GCAGGCCAGGCCAG
 TGAGGGAAACAGCAAGGGCAGGTATCACAGCCTGGAGACACCC
 ACAGATGGCTGGATCCGGTGCTACGG
 ACATTTCTAAGATGCCCATGAGAACAGACAGAACAGATGT
 GTACAGCACTATGAGCATT
 TAAACACCTCCAGAAT
 CAATAATCGTGGCAACATATCTCTGTA
 AAAACAAACACTGTA
 ACTTCTAAATAATGTTAGTCTCCCTGTA
 AAAA

FIGURE 36

MLRGTMATWRGMRPEVTLACLLATAGCFADLNEVPQVTVQPASTVQKPGGTIVLGVVEPP
 RMNVTWRLNGKELNGSDDALGVLITHGTLVITALNNHTVGRYQCVARMPAGAVASVPATVTL
 ANLQDFKLDVQHVIEVDEGNTAVIACHLPESHPKAQVRYSVKQEWEASRGNYLIMPSGNLQ
 IVNASQEDEGMYKCAAYNPVTQEVKTSGSSDRLVRSTAEEAARIIYPPEAQTIIVTKGQSL
 ILECVASGIPPPRVTWAKDGSSVTGYNKTRFLLSNLLIDTTSEEDSGTYRCMADNGVGQPGA
 AVILYNVQVFEPPEVTMELSQLVIPWGQSAKLTCERGNPPPSVLWLRNAVPLISSQRRLS
 RRALRVLSMGPEDEGVYQCMAENEVGSAHAVVQLRTSRPSITPRLWQDAELATGTPPVSPSK
 LGNPEQMLRGQPALPRPPTSVGAPSPKCPGEKGQGAPAEAPIILSSPRTSKTDSYELVWRPR
 HEGSGRAPILYVVVKHRKQVTNSSDDWTISGI PANQHRLTLTRLDPGSLYEVEMAAYNCAGE
 GQTAMVTFRTRGRRPKPEIMASKEQQIQRDDPGASPQSSQPDHGRLSPPEAPDRPTISTASE
 TSVYVTWI PRGNGGFPIQSFRVEYKKLKVGDWILATS AIPPSRLSVEITGLEKGTSYKFRV
 RALNMLGESEPSAPS RPYVVSGYSGRVYERPVAGPYITFTDAVNETTIMLKWMYIPASNNNT
 PIHGFYIYYRPTSDNDSDYKKDMVEGDKYWH SISHLQPETSYDIKMQCFNEGGESEFSNVM
 ICETKARKSSGQPGRLPPPTLAPPQPLPETIERPVGTGAMVARSSDPYLVGVVLGSIVL
 II VTFIPFCLWRAWSKQKHTDLGFPRSA LPPSCP YTMVPLGGLPGHQASGQPYLSGISGRA
 CANGIHMNRGCP SAAVGYPGMKPQQHCPGELQQQSDTSLLRQTHLGNGYDPQSHQITRGPK
 SSPDEGSFLYTL PDDSTHQLLQPHDCCQRQE QPAAVGQSGVRRAPDSPVLEAVWDPPFHSG
 PPCCLGLVPVEEVDS PDSCQVSGGDWCPQHPVGAYVGQEPGMQLSPGPLVRVSFETPPLTI

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 16-30 (type II), 854-879

FIGURE 37

CGGGAGGCTGGTCGTATGATCCGGACCCATTGTCGGCCTCTGCCATGCCTGCTCCTC
 CCAGGCTCCCGCGGCCGACCCCCGCGCAAC**ATG**CAGCCCACGGGCCGAGGGTTCCCGCGC
 GCTCAGCCGGCGGTATCTGCGCGTCTGCTCCTGCTACTGCTGCTGCTGCGGAGC
 CCGTAACCCGCGCGAGACCACGCCGGCGCCCCAGAGCCCTCTCACGCTGGGCTCCCC
 AGCCTCTTACCAACGCCGGGTGTCCCCAGGCCCTCACTACCCAGGCCTCACTAGCCAGG
 CACCCCCAAACCTGGACCTCGGGTCGCGCGAGGCCCTGATGCGGAGTTCCACTCG
 TGGACGGCCACAATGACCTGCCAGGTCTGAGACAGCGTTACAAGAATGTGCTTCAGGAT
 GTTAACCTGCGAAATTTCAGCCATGGTCAGACCAGCCTGGACAGGCTTAGAGACGGCCTCGT
 GGGTGCCAGTTCTGGTCAGCCTCCGTCTCATGCCAGTCCCAGGACCAGACTGCCGTGCGCC
 TCGCCCTGGAGCAGATTGACCTCATTCACCGCATGTGTGCCCTACTCTGAACCTGAGCTT
 GTGACCTCAGCTGAAGGTCTGAACAGCTCTCAAAGCTGGCCTGCCCTATGGCGTGNAGGG
 TGGTCACTCACTGGACAGCAGCCTCTGTGCTGCGCAGTTCTATGTGCTGGGGTGCCT
 ACCTGACACTTACCTCACCTGCAGTACACCAGGGCAGAGAGTCCACCAAGTTCAGACAC
 CACATGTACACCAACGTCAAGGGATTGACAAGCTTGGTGAGAAAGTAGTAGAGGGAGTTGAA
 CCGCCTGGCATGATGATAGATTGTCCATGCATGGACACCTTGATAAGAAGGGCCTGG
 AAGTGTCTCAGGCTCCTGTGATCTTCTCCACTCAGCTGCCAGAGCTGTGTGACAATTG
 TTGAATGTTCCCGATGATATCCTGCAGCTCTGAAGAACGGTGGCATCGTGTGACACT
 GTCCATGGGGTGCAGTCAACCTGCTGCTAACGTGTCCACTGTGGCAGATCACTTG
 ACCACATCAGGGCAGTCATTGGATCTGAGTTCATGGGATTGGTGGAAATTATGACGGGACT
 GGCGGTTCCCTCAGGGCTGGAGGATGTGTCCACATACCCAGTCCTGATAGAGGGAGTTGCT
 GAGTCGTASCTGGAGCAGGAAGAGCTTCAAGGTGTCCCTCGTGGAAACCTGCTGCGGGTCT
 TCAGACAAGTGGAAAAGGTGAGAGAGGGAGAGCAGGGCGCAGAGCCCCGTGGAGGCTGAGTT
 CCATATGGCAACTGAGCACATCCTGCCACTCCCACCTCGTCCCTCAGAATGGACACCCAGGC
 TACTCATCTGGAGGTGACCAAGCAGCCAACCAATGGGCTCCCTGGAGGCTCAAATGCCT
 CCCCATACCTTGTCCAGGCCTTGTGGCTGCCACCATCCAACCTCACCCAGTGGCTC
TGCTGACACAGTCGGTCCCCGAGAGGTCACTGTGGCAAAGCCTCACAAAGCCCCCTCCT
 AGTTCATTACAAGCATATGCTGAGAATAACATGTTACACATGGAAAA

FIGURE 38

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817
><subunit 1 of 1, 487 aa, 1 stop, 2 unknown
><MW: 53569.32, pI: 7.68, NX(S/T): 5
MQPTGREGSRALSRRRLLLLLLRLQPVTRAETTPGAPRALSTLGSPSLFTTPGVPS
ALTPGLTPGTPKTLRGRAQALMRSFPLVDGHNDLPQVLQRYKNVLQDVNLRNFSHGQ
TSLDRLRDGLVGAQFWASAVSCQSQDQTAVRLALEQIDLIHRMCASYSELELVTSAEGLNSS
QKLACLIGVXGGHSILDSSLVLSFYVLGVRYLTLTFTCSTPWAESSTKFRHHMYTNVSGLT
SFGEKVVEELNRLGMMIDLSYASDTLIRRLEVSQAPVIFSHSAARAVCDNLLNPDDILQL
LKNGGIVMVTLSMGVLQCNLLANVSTVADHFDHIRAVIGSEFIGIGGNYDGTGRFPQGLEDV
STYPVLIEELLSRXWSEEELQGVLRGNLLRVFRQVEKvreesRAQSPVEAEFPYQQLSTSCH
SHLVPQONGHQATHLEVTKQPTNRVPWRSSNASPYLVPGLVAAATIPTFTQWLC
```

Important features of the protein:

Signal peptide:

amino acids 1-36

Transmembrane domain:

amino acids 313-331

N-glycosylation sites.

amino acids 119-122, 184-187, 243-246 and 333-336

N-myristoylation sites.

amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359, 357-362, 394-399, 427-432 and 472-477.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 136-146

FIGURE 39

TGCTAGGCTCTGTCCCACAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGA
 TCCCTCTATGACTGCAATGTGAGGTGTCCGGCTTGCTGGCCCAGCAAGCCTGATAAGC**ATG**
 AAGCTCTTATCTTGGTGGCTGTGGTGGGTGTTGCTGGTGCCAGCTGAAGCCAACAA
 GAGTTCTGAAGATATCCGGTGCAAATGCATCTGTCCACCTTATAGAAACATCAGTGGCACA
 TTTACAACCAGAATGTATCCCAGAAGGACTGCAACTGCCTGCACGTGGTGGAGCCATGCCA
 GTGCCTGGCCATGACGTGGAGGCCTACTGCCTGCTGTGCGAGTGCAGGTACGAGGAGCGCAG
 CACCACCACCATCAAGGTATCATTGTATCTACCTGTCCGTGGTGGGTGCCCTTTGCTCT
 ACATGGCCTTCCTGATGCTGGTGGACCCCTGTATCCGAAAGCCGGATGCATACACTGAGCAA
 CTGCACAATGAGGAGGAGAATGAGGATGCTCGCTATGGCAGCAGCTGCTGCATCCCTCGG
 GGGACCCCGAGCAAACACAGTCCTGGAGCGTGTGGAAGGTGCCAGCAGCGGTGGAAGCTGC
 AGGTGCAGGAGCAGCGGAAGACAGTCTCGATGGCACAAAGATGCTCAG**TAG**ATGGGCTGG
 TGTGGTTGGGTCAAGGCCAACACCATGGCTGCCAGCTCCAGGCTGGACAAAGCAGGGGG
 CTACTTCTCCCTTCCCTCGGTTCCAGTCTTCCCTTAAAGCCTGTGGCATTTCCTCCTT
 CTCCCTAACTTAGAAATGTTGACTTGGCTTTGATTAGGGAAAGAGGGATGTGGTCTCT
 GATCTCTGTTGTTCTTGGGCTTTGGGTTGAAGGGAGGGGAAGGCAGGCCAGAAGGGA
 ATGGAGACATTGAGGCGGCCTCAGGAGTGGATGCGATCTGTCTCCCTGGCTCCACTCTT
 CCGCCTCCAGCTCTGAGTCTGGGAATGTTTACCTGGAAAGATAAAGCTGGGCTTCA
 GGAACTCAGTGTCTGGGAGGAAAGCATGGCCAGCATTGAGCATGTGTTCTTCTGCAGTG
 GTTCTTATCACCACCTCCCTCCAGCCCCGGCCTCAGCCCCAGCCCCAGCTCCAGCCCTG
 AGGACAGCTCTGATGGGAGAGCTGGGCCCCCTGAGCCCAGTGGCTTCAGGGTGCAGTGG
 AGCTGGTGTTCGCTGTCCCCTGTGCACTTCTCGCACTGGGCATGGAGTGCCATGCATACT
 CTGCTGCCGGTCCCCCTCACCTGCACTTGAGGGGCTGGCAGTCCCTCTCCCCAGTGTGTC
 CACAGTCACTGAGCCAGACGGTCGGTTGGAACATGAGACTCGAGGCTGAGCGTGGATCTGAA
 CACCACAGCCCCCTGTACTTGGGTTGCCTTGTCCCTGAACCTCGTTGACCGATGGA
 GAGAAAATTGTCCTTGTCTTAGAGTTGTGTAAATCAAGGAAGCCATCATTAAATTG
 TTTTATTCCTCTCA

FIGURE 40

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278
<subunit 1 of 1, 183 aa, 1 stop
<MW: 20574, pI: 6.60, NX(S/T): 3
MKLLSLVAVVGCLLVPPAEANKSSEDIRCKCICPPYRNISGHYNQNVSQKDCNCLHVVEPM
PVPGHDVEAYCLLCECRYEERSTTIKVIIVIYLSVVGALLLYMAFLMLVDPLIRKPDAYTE
QLHNEEENEDARSMAAAASLGGPRANTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS
```

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 90-112

N-glycosylation sites.

amino acids 21-24, 38-41 and 47-50

FIGURE 41

AGCGGGTCTCGCTTGGGTCCGCTAATTCTGCCTGAGGCGTGAGACTGAGTCATAGGGTCTGGTCCCCGA
 ACCAGGAAGGGTTGAGGAACACAATCTGCAAGCCCCCGCACCAAGTGAGGGGCCCGTGTGGGTCTCCC
 TCCCTTGCATTCCCACCCCTCCGGGCTTGCCTCTTCCGGGACCCCTGCCGGGAG**ATG**GCCGGTTGATG
 CGGAGCAAGGATTGCTCTGCTCCTACTGGCCGGTGTGATGGTGGAGAGCTCACAGATCGGCAGT
 TCGGGGCCAAACTCAACTCCATCAAGTCCTCTGGGGAGACGCCGGTGTGAGGCCAACATCGATCTGCG
 GGCATGTACCAAGGACTGGCATTCGGCGCAGTAAGAAGGGCAAAAACCTGGGGCAGGCCAACCTTGTAGCAGT
 GATAAGGAGTGTGAAGTGGGAGGTATTGCCACAGTCCCCACCAAGGATCATGGCCTGATGGTGTGGAGA
 AAAAGAAGCGCTGCCACCGAGATGGCATGTGCTGCCAGTACCCGCTGCAATAATGGCATCTGTATCCAGT
 ACTGAAAGCATCTAACCCCTCACATCCGGCTGGATGGTACTCGGCACAGAGATCGAAACCACGGTATTAC
 TCAAACCATGACTTGGGATGGCAGAATCTAGGAAGACACACACTAAGATGTACATATAAAAGGGCATGAAGGA
 GACCCCTGCCACGATCATCAGACTGCATTGAAGGGTTTGCTGTGCTCGTACCTGGACCAAAACTGCAAA
 CCAGTGCTCCATCAGGGGAAGTCTGACCAAACAAGCAAGAAGGGTCTCATGGGCTGAAATTTCAGCGT
 TGCGACTGTGCGAAGGGCCTGCTTGCAAAGTATGGAAAGATGCCACCTACTCCTCAAAGCCAGACTCCATGTG
 TGTCAGAAAAATT**TGAT**CACCATGGAGAACATCATCAATTGCAGACTGTGAAGTTGTGTATTAAATGCATTATAG
 CATGGTGGAAAATAAGGTCAGATGCAGAAGAATGGCTAAAATAAGAAACGTGATAAGAATATAGATGATCACAA
 AAAGGGAGAAGAAAACATGAACGTAAATAGATTAGAATGGGTGACAAATGCAGTGAGCCAGTGTCCATTATG
 CAACTGTCTATGTAATAATGTACACATTGTGAAAATGCTATTATAAGAGAACAGCACAGTGGAAATT
 ACTGATGAGTAGCATGTGACTTCCAAGAGTTAGGTTGTGCTGGAGGAGAGGTTCTCAGATTGCTGATTGC
 TTATACAAATAACCTACATGCCAGATTCTATTCAACGTAGAGTTAACAAAATACTCCCTAGAATAACTTGT
 TACAATAGGTTCTAAAATAATTGCTAAACAAGAAATGAAAACATGGAGCATGTTAATTACAAACAGAAAAT
 TACCTTTGATTTGTAACACTACTTCTGCTGTCATCAAGAGTCTGGTAGATAAGAAAAAAATCAGTCATAT
 TTCCAAATAATTGCAAAATAATGCCAGTTGTTAGGAAGGCCTTTAGGAAGAACAAATAACAAACAAACAG
 CCACAAATAACTTTTTCAAAATTAGTTACCTGTAATTAAAGAACGTGATAACAGACAAAACAGTTCC
 TTCAAGATTCTACGGAATGACAGTATCTCTTCTTATCCTATGTGATTCTGCTCTGAATGCAATTATTTCCA
 AACTATACCCATAAAATTGTGACTAGTAAATACTTACACAGAGCAGAATTTCACAGATGGCAAAAATTTAA
 GATGTCATATGTTGAAAAGAGCTAACAGAGAGATCATTATTCTAAAGGATTGGCCATAACCTATATT
 GATAGAATTAGATTGTTAATACATGTATTACATACACTCTGTGTTAATAGAGACTTAAGCTGGATCTGTACTG
 CACTGGAGTAAGCAAGAAAATTGGAAAACCTTTGTTGTTCAAGGTTGGCAACACATAGATCATATGTCTG
 AGGCACAAGTTGGCTGTCATTTGAAACCAAGGGATGCCAGTCTAAATGAATATCTGCATGGGATTGCTAT
 CATAATATTACTATGCAGATGAATTCACTGAGGTCTGTGCTGCTACTATCCTCAAATTATTATTTATAG
 TGCTGAGATCCTCAAATAATCTCAATTTCAGGAGGTTCACAAAATGTAACCTGAGTAGACAGAGTAGTGAGG
 TTTCATTGCCCTCTATAAGCTCTGACTAGCCAATGGCATCATCCAATTTCCTCCAAACCTCTGCAGCATCTG
 CTTTATTGCCAAAGGGCTAGTTGGTTCTGCAGGCCATTGCCATTGGTTAAAAAATATAAGTAGGATAACTGTAAA
 ACCTGCATATTGCTAATCTATAGACACCACAGTTCTAAATTCTTGAAACCACCTTACTACTTTTTAAACTT
 AACTCAGTTCTAAATACTTGTCTGGAGCACAAAACAATAAAAGGTATCTTATAGTCGTGACTTAAACTTTG
 TAGACCACAATTCACTTTAGTTCTTTACTTAAATCCATCTGAGTCATCAAATTAAAGTTCTCCAGTAG
 AGATTGAGTTGAGCCTGTATATCTATTAAAATTCAACTTCCCACATATATTACTAAGATGATTAAGACTTA
 CATTTCAGTCACAGGTCTGCAAAACAAAATATAAACTAGTCCATCCAAGAACCAAGTTGTATAAAACAGGT
 TGCTATAAGCTGTGAAATGAAACATTCAATCAAACATTCTCTATATAACAATTATTATTTACAAT
 TTGGTTCTGCAATTATTCTTATGTCCACCCCTTTAAAATTATTATTTGAAGTAATTATTACAGGAAATG
 TTAATGAGATGTATTCTTATAGAGATATTCTTACAGAAAGCTTGTAGCAGAATATATTGCAGCTATTGAC
 TTTGTAATTAGGAAAATGTATAAAAGATAAAACTTAAATTCTCCTCTAAACACTGAAAAAA
 AAAAAAAAAAAAAAA

FIGURE 42

MAALMRSKDSSCCLLLAAVLMVESSQIGSSRAKLSNIKSSLGGETPGQAANRSAGMYQGLA
FGGSKKGKNLGQAYPCSSDKECEVGRYCHSPHQGSSACMVCRKKRCHRDGMCCPSTRCNN
GICIPVTEISILTPHIPALDGTRHRDRNIGHYSNHDLGWQNLGRPHTKMSHIKGHEGDPLRS
SDCIEGFCCARHFWTICKPVLHQGEVCTKQRKKGSHGLEIFQRCDCAKGLSCKVWKDATYS
SKARLHVCQKI

Signal peptide:

amino acids 1-25

FIGURE 43

TCTCAATCTGCTGACCTCGT GATCCGCCTGACCTTGT AATCCACCTACCTGGCCTCCAAA
 GTGTTGGGATTACAGGCGTGAGCCACCGCGCCGGCAACATCACGTTTAAAAATTGATT
 TCTTCAAATT CATGGCAAATATTCCTCCCTTAACCTCTATGTCAGAATGAGGAAGGA
 TAGCTGCATTATTAGTCAGTTTCATTGCATAGTAATATTCATGTAGTATTCTAAG
 TTATATTTAGTAATT CATATGTTAGATTAGGTTAACATACTTGTGAAAATACTG
ATGTGTTTAAAGCCTGGGCAGAAATTCTGTATTGTTGAGGATTGTTCTTTATCCCCCT
 TTTAAAGTCATCCGTCCTGGCTCAGGATTGGAGAGCTGCACCACCAAAATGGCAAACA
 TCACCAAGCTCCCAGATTTGGACCAGTTGAAAGCTCCGAGTTGGGCCAGTTACCACCACC
 CCAAGTACACAGCAGAATAGTACAAGTCACCCTACAACACTACTACTTCTTGGGACCTCAAGCC
 CCCAACATCCCAGTCCTCAGTCCTCAGTCATCTGACTCAAATCTCAACCTGAGCCATCCC
 CAGTTCTTAGCCAGTTGAGCCAGCGACAACAGCACCAGAGCCAGGCAGTCAGTCACTGTTCTCCT
 CCTGGTTGGAGTCCTTCCTCCAGGCAGAAACTTCGAGAATCAACACCTGGAGACAGTCC
 CTCCACTGTGAACAAGCTTGCAGCTCCAGCAGCACCATTGAAAATATCTGTGCTG
 TCCACCAGCCACAGCCAAACACATCAAACCTGCTAACGGCGGATACCCCCAGCTCTAAG
 ATCCCAGCTCTGCAGTGGAAATGCCTGGTCAGCAGATGTCACAGGATTAAATGTGCAGTT
 TGGGGCTCTGGAATTGGGTCAAGAACCTCTCTCTGAATTGGATCAGCTCCAAGCAGTG
 AAAATAGTAATCAGATTCCATCAGCTGTATTGAAGTCTTAAGTGAGCCTTGAATACA
 TCTTATCAATGACCAGTGCAGTACAGAACTCCACATATACAACCTCCGT CATTACCTCCTG
 CAGTCTGACAAGCTCATCACTGAATTCTGCTAGTCCAGTAGCAATGTCTTCTTATGACC
 AGAGTTCTGTGCATAACAGGATCCCATAACAAAGCCCTGTGAGTTCATCAGAGTCAGCTCCA
 GGAACCACATCATGAATGGACATGGTGGTGGTCGAAGTCAGCAGACACTAGACAGTAAGTATAG
 CAGCAAGCTACTCTGTATGGCTGGGCCAACAAACAGAGGAAGAGGATAGCTACGTGA
 TGTGGAAAACACCAGTTGGTCATGGCTGGCTCATTGCT**TAA**AAAGCAGCCCTTTGCTTTTGT
 TTTGGACCAGGTGTTGGCTGTGGTTATTAGAAATGTCTTAACCACAGCAAGAAGGAGGT
 GGTGGTCTCATATTCTCTGCCCTAATCAGACTGCACCACAAGTGCAGCATACTAGTGCAT
 TTTAAAGATGCTTGGCCAGGCAGGGTGGCTGATGCCATAATCCAGTGCTTGGGGGCC
 AAGGCAGGCAGATTGCCAAGCTCAGGAGTTGAGACCACCCCTGGCAACATGGTAAACTC
 TGTCTACTAAAATACGAAAAACTAGCCGGGTGTGGTGGCGCGCGTGCCTGTAATCCCAG
 CTACTTGGGAGGCTGAGGCACAAGAATCGCTTGAGCCAGCTTGGCTACAAAGTGAGACTCC
 GTCTGAAAAGA

FIGURE 44

MCFKALGRNSVLLRICSFIPPLKSSVLGSGFGEAPPKMANITSSQILDQLKAPSLGQFTTT
PSTQQNSTSHPTTTSWDLKPPTSQSSVLSHLDFKSQPEPSPVLSQLSQRQQHQSQAVTVPP
PGLESFPSQAKLRESTPGDSPSTVNKLQLPSTTIENISVSVHQQPQPKHIKLAKRRIPPASK
IPASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSAPSSENSNQIPISLYSKSLSEPLNT
SLSMTSAVQNSTYTTSVITSCSLTSSLNSASPVAMSSSYDQSSVHNRIPYQSPVSSSESAP
GTIMNGHGGGRSQQTLD SKYSSKLLSWLVPTKQRKRIA HVMWKT PVGQWLIR

Signal peptide:

amino acids 1-24

FIGURE 45

GCCGAGTGGGACAAAGCCTGGGCTGGCGGGGCC **ATG** GCGCTGCCATCCGAATCCTGCT
 TTGGAAACTTGTGTTCTGCAGAGCTTGCTGTTCTCCTGCACTCAGCGGTGGAGGAGACGG
 ACGCGGGCTGTACACCTGCAACCTGACCACATCACTACTGCCACCTTACGAGAGCCTGGCC
 GTCCGCCTGGAGGTACCGACGGCCCCCGGCCACCCCGCCTACTGGGACGGCGAGAAGGA
 GGTGCTGGCGGTGGCGCGCGCACCGCGCTTCTGACCTGCGTAACCGCGGGCACGTGT
 GGACCGACCGGCACGTGGAGGAGGCTAACAGGTGGTGCACGGGACCGGCAGCCGCCGGG
 GTCCCGCACCGCGCGGACCGCCTGCTGGACCTTACCGTCGGCGAGCGCCGCCCTA
 CGGGCCCCTTTCTGCGCGACCGCGTGGCTGTGGCGGGATGCCCTTGAGCGCGGTGACT
 TCTCACTGCGTATCGAGCCGCTGGAGGTCGCGACGAGGGCACCTACTCCTGCCACCTGCAC
 CACCAATTACTGTGGCCTGCACGAACGCCCGTCTTCCACCTGACGGTCGCCAACCCACGC
 GGAGCCGCCCGGGCTCTCCGGCAACGGCTCCAGCCACAGCGGCCAGGCCAG
 ACCCCACACTGGCGCGGCCACAACGTATCAATGTATCGTCCCCGAGAGCCGAGCCCAC
 TTCTTCCAGCAGCTGGCTACGTGCTGGCACGCTGCTGCTTCACTGCTACTGGTCAC
 TGTCCCTGGCCGCCCGCAGGCGCCGGAGGCTACGAATACTCGGACCAGAAGTCGGAA
 AGTCAAAGGGAAAGGATGTTAACTTGGCGGAGTTCGCTGTGGCTGCAGGGGACCAGATGCTT
 TACAGGAGTGAGGACATCCAGCTAGATTACAAAAAACATCCTGAAGGAGAGGGCGGAGCT
 GGCCACAGCCCCCTGCCCTGCCAAGTACATCGACCTAGACAAAGGGTCCGAAGGAGAACT
GCAAATAGGGAGGCCCTGGCTCCTGGCTGGCTGGCCAGCAGCTGCACCTCTCCTGTCTGCTC
 CTCGGGCATCTCCTGATGCTCCGGGCTCACCCCTCCAGCGGCTGGTCCCCTTCC
 GGAATTGGCCTGGCGTATGCAGAGGCCCTCACACCCCTCCCCAGGGCTTGGTGGC
 AGCATAGCCCCACCCCTGCCCTTGCTCACGGTGGCCCTGCCACCCCTGGCACAAACC
 AAAATCCCACGTGCCCACATGCCCTCAGACCCCTCTGGCTCTGCCGCTGGGGCCTG
 AAGACATTCTGGAGGACACTCCATCAGAACCTGGCAGCCCCAAAACGGGTCAACCTCA
 GGGCAGGAGTCCCACCTCCAGGGCTCTGCTCGTCCGGGCTGGAGATGTTCTGGAGGA
 GGACACTCCCACATCAGAACCTGGCAGCCTGAAGTTGGGTCAACCTCGGCAGGAGTCCCAC
 CCTCCTGGGTGCTGCCTGCCACCAAGAGCTCCCCACCTGTACCAACCATGTGGACTCCAG
 GCACCATCTGTTCTCCCCAGGGACCTGCTGACTGAATGCCAGCCCTGCTCCTGTGTTG
 CTTGGGCCACCTGGGCTGCACCCCTGCCCTTCTGCCCATCCCTACCCCTAGCCTTG
 CTCTCAGCCACCTTGATAGTCAGGGCTCCCTGTGACTTCTGACCCCTGACACCCCTCC
 GGACTCTGCCTGGGCTGGAGTCTAGGGCTGGGCTACATTGGCTTCTGACTGGCTGAGGA
 CAGGGGAGGGAGTGAAGTTGGTTGGGTGCCACTCTCAGCACCCACATT
 GCATCTGCTGGTGGACCTGCCACCATCACAATAAGTCCCCATCTGATTTAAAAAAAA
 AAAAAA

FIGURE 46

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60618
<subunit 1 of 1, 341 aa, 1 stop
<MW: 38070, pI: 6.88, NX(S/T): 1
MALPSRILLWKLVLQSSAVLLHSAVEETDAGLYTCNLHHHYCHLYESLAVRLEVTDGPPAT
PAYWDGEKEVLA VARGAPALLTCVNRGHVWTDRHVEEAQQVVHWRQPPGVPHDRADRLLDL
YASGERRAYGPLFLRDRVAVGADA FERGDFSLRIE PLEVADEGTYSCHLHHHYCGLHERRVF
HLTVAE PHAE PPPRGSPGNGSSHSGAPGP DPTLARGHNVINVIVPESRAHFFQQLGYVLATL
LLFILLLVTLAARRRRGGYEYSDQKSGKSKGDVNLA EFAVAAGDQMLYRSEDIQLDYKN
NILKERAELAHSPLPAKYIDL DKGFRKENCK
```

Important features:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 237-262

N-glycosylation site.

amino acids 205-208

Cell attachment sequence.

amino acids 151-154

Coproporphyrinogen III oxidase proteins.

amino acids 115-140

FIGURE 47

CGCCGGAGGCAGCGGCCGTGGCGCAGCGCGAC**ATG**GCCGTTCTCAGAGGACGACTT
 CAGCACAGTCAAACCTCACGGAACCACAAGCAGCAGTCTCGAGCTGACCAGGAGGC
 ACTGCTTGAGAAGCTGCTGGACCGCCCCCTGGCCTGCAGAGGCCGAGGACCGCTTCT
 GTGGCACATACATCATCTTCTCAGCCTGGGATTGGCAGTCTACTGCCATGGAACCTCTT
 ATCACTGCCAAGGAGTACTGGATGTTCAAACCTCGCAACTCCTCAGCCCAGCCACGGGA
 GGACCCCTGAGGGCTCAGACATCCTGAACACTTGGAGAGCTACCTTGCCTGCCACCC
 TGCCCTCCATGCTGTGCCTGGCCAACCTCCTGCTTCAACAGGGTTGCAGTCACATC
 CGTGTCTGGCCTCACTGACGGTACCTGGCCATCTCATGGTATAACTGCACTGGTGA
 GGTGGACACTTCCTCCTGGACCCGTGGTTTTTGCGGTACCAATTGTCTGCATGGTATCC
 TCAGCGGTGCCTCCACTGTCTCAGCAGCAGCATCTACGGCATGACCGGCTCCTTCTATG
 AGGAACCTCCAAGCACTGATATCAGGAGGAGCCATGGGCGGGACGGTCAGCGCCGTGGCCTC
 ATTGGTGGACTTGGCTGCATCCAGTGATGTGAGGAACAGCGCCCTGGCCTCTTGTGACGG
 CCACCATCTCCTCGTCTGCATGGACTCTACCTGCTGTCCAGGCTGGAGTATGCC
 AGGTAACATGAGGCCTGTTCTGCGGCCATGTGTTTCTGGTGAAGAGGAGCTCC
 GGACTCCCTCAGTGCCCTTCGGTGGCCTCCAGATTGATTCCCACACACCCCTCTCC
 GCCCCATCTGAAGAACAGGCCAGCCTGGCTCTGTGTCACCTACGTCTTCTCATCACC
 AGCCTCATCTACCCCGCGTCTGCACCAACATCGAGTCCTCAACAAGGGCTGGGCTCACT
 GTGGACCACCAAGTTTCATCCCCCTCACTACCTTCCCTGTACAACATTGCTGACCTAT
 GTGGCCGGCAGCTCACCGCTGGATCCAGGTGCCAGGGCCAACAGCAAGGCCTCCAGGG
 TTCGTGCTCTCCGGACCTGCCTCATCCCCCTTCTGCTCTGTAACTACCAGCCCCCGT
 CCACCTGAAGACTGTGGTCTCCAGTCCGATGTGTAACCCGCACCTCAGCTCCCTGCTGG
 GGCTCAGCAACGGCTACCTCAGCACCCCTGGCCCTCTACGGGCTAAGATTGTGCCAGG
 GAGCTGGCTGAGGCCACGGGAGTGGTATGTCCTTTATGTGTGCTTGGGCTAACACTGGG
 CTCAGCCTGCTCACCTCCTGGTGCACCTCATC**TAG**AAGGGAGGACACAAGGACATTGGT
 CTTCAGAGCCTTGAAGATGAGAAGAGAGTGCAGGAGGGCTGGGGCCATGGAGGAAGGCC
 TAAAGTTCACTTGGGACAGAGAGCAGAGCACACTCGGGCCTCATCCCTCCAAGATGCCA
 GTGAGCCACGTCCATGCCATTCCGTCAAGGCAGATAATTCCAGTCATATTAAAGAACACT
 CCTGAGACAGTTGAAGAAGAAATGACAAATCAGGGTACTCCCTCACAGCTGATGGTTA
 ACATTCCACCTTCTTCTAGCCCTCAAAGATGCTGCCAGTGTGCTGCCCTAGAGTTATTACA
 AAGCCAGTGCCAAAACCCAGCCATGGGCTTTGCAACCTCCAGCTGCGCTATTCCAGCT
 GACAGCGAGATGCAAGCAAATGCTCAGCTCCTTACCCCTGAAGGGGTCTCCCTGGAATGGA
 AGTCCCCTGGCATGGTCAGTCCTCAGGCCAAGACTCAAGTGTGCACAGACCCCTGTGTTCT
 GCAGGGTGAACAACGTCCCCTAACCAAGACTGGAAAACCCAGAAAGATGGGCCTCCATGAAT
 GCTTCATTCCAGAGGGACCAAGAGGGCTCCCTGTGCAAGGGATCAAGCATGTCTGGCCTGGG
 TTTCAAAAAAAAGAGGGATCCTCATGACCTGGTGGTCTATGGCCTGGGCTAAGATGAGGGTC
 TTTCAGTGTCTGTTACAACATGTCAGCCATTGGTTCAAGGGCGTAATAAATACTTGC
 GTATTCAAAAA

FIGURE 48

MAVVSEDDFQHSSNSTYGTTS defense protein
GSLLPWNNFFITAKEYWMFKLRNSSSPATGEDPEGSDILNYFESYLAVASTVPSMLCLVANFL
LVNRVAVHIRVLASLTVILAIFMVITALVKVDTSSWTRGFFAVTIVCMVILSGASTVFSSSI
YGMTGSFPMRNSQALISGGAMGGTVSAVASLVDLAASSDVRNSALAFFLTATIFLVLCMGLY
LLLRSRLEYARYYMRPVLAHVFSGEELPQDSLSAPSVASRFIDSHTPPLRPILKKTASLGF
CVTYVFFITSЛИYPAVCTNIESLNKGSGSLWTTKFFIPLTFLLYNFADLCGRQLTAWIQVP
GPNSKALPGFVLLRTCLIPLFVLCNYQPRVHLKTVVFQSDVYPALLSLLGLSNGYLSTLAL
LYGPKIVPRELAEATGVVMSFYVCLGLTLGSACSTLLVHLI

Transmembrane domain:

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252,
305-330, 448-472

FIGURE 49

GACAGTGGAGGGCAGTGGAGAGGACCGCGCTGTCCTGCTGTCACCAAGAGCTGGAGACACCA
 TCTCCCACCGAGAGTCATGCCCCATTGGCCCTGCACCTCCTCGTCCTCGTCCCCATCCTCC
 TCAGCCTGGTGGCCTCCCAGGACTGGAAGGCTGAACGCAGCCAAGACCCCTCGAGAAATGC
 ATGCAGGATCCTGACTATGAGCAGCTGCTCAAGGTGGTACCTGGGGCTCAATCGGACCT
 GAAGCCCCAGAGGGTATTGTGGTGGCGCTGGTGTGGCCGGCTGGTGGCCGCCAAGGTGC
 TCAGCGATGCTGGACACAAGGTACCATCCTGGAGGCAGATAACAGGATCGGGGCCGCATC
 TTCACCTACCGGGACCAGAACACGGCTGGATTGGGAGCTGGAGCCATGCGATGCCAG
 CTCTCACAGGATCCTCCACAAGCTCTGCCAGGGCCTGGGGCTAACCTGACCAAGTTCACCC
 AGTACGACAAGAACACGTGGACGGAGGTGCACGAAGTGAAGCTGCGCAACTATGTGGTGGAG
 AAGGTGCCCGAGAACAGCTGGCTACGCCCTGCCTCCCCAGGAAAAGGCCACTGCCCGAAGA
 CATCTACCAAGATGGCTCTCAACCAGGCCCTCAAAGACCTCAAGGCACTGGGCTGCAGAAAGG
 CGATGAAGAACAGTTGAAAGGCACACGCTCTTGAATATCTTCTCGGGAGGGAACCTGAGC
 CGGCCGGCCGTGCAGCTCTGGAGACGTGATGTCCGAGGATGGCTTCTTATCTAGCTT
 CGCCGAGGCCCTCCGGGCCACAGCTGCCCTAGCGACAGACTCCAGTACAGCCGCATCGTGG
 GTGGCTGGGACCTGCTGCCCGCGCTGCTGAGCTCGCTGTCCGGCTTGTGCTGTTGAAC
 GCGCCCGTGGTGGCAGACCCAGGGACCGCACGATGTGCACGTGCAGATCGAGACCTCTCC
 CCCGGCGCGGAATCTGAAGGTGCTGAAGGCCACGTGGTGTGCTGACGGCGAGCGGACCGG
 CGGTGAAGCGCATCACCTCTGCCGCCGCTGCCCGCACATGCAGGAGGCCTGCGGAGG
 CTGCACTACGTGCCGCCACCAAGGTGTTCTAACGCTTCCGCAGGCCCTCTGGCGCGAGGA
 GCACATTGAAGGCGCCACTCAAACACCGATGCCCGCGCATGATTTCTACCCGCCGC
 CGCGCGAGGGCGCGCTGCTGGCCTCGTACACGTGGCGACGCCGGCAGCGTTCGCC
 GGCTTGAGCCGGGAAGAGGCCTTGCCTGGCGCTCGACGACGTGGCGGCATTGCACGGGCC
 TGTCGTGCCAGCTCTGGACGGCACCGCGCTCGTCAAGCGTTGGCGAGGACCGACA
 GCCAGGGTGGCTTGTGGTACAGCCGCCGGCCTCTGGCAAACCGAAAAGGATGACTGGACG
 GTCCCTTATGGCCGCATCTACTTGCCTGGCAGCACCCGCTACCCGCACGGCTGGTGGGA
 GACGGCGGTCAAGTCGGCGCTGCCGCCATCAAGATCAACAGCCGAAGGGGCCTGCAT
 CGGACACGCCAGCCCCGAGGGGCACGCATCTGACATGGAGGGCAGGGCATGTGCATGGG
 GTGGCCAGCAGCCCTCGCATGACCTGGCAAAGGAAGAAGGCAGCCACCCCTCCAGTCCAAGG
 CCAGTTATCTCCAAAACACGACCCACACGAGGACCTCGCATTAAAGTATTTGGAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 50

MAPLALHLLVLVPILLSLVASQDWKAERSQDPFEKCMQDPDYEQLLKVVTWGLNRTLKPQRV
IVVGAGVAGLVAAKVLSAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSHRL
HKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKPEKLGYALRPQEKGHSPEDIYQMA
LNQALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRAVQLLGDMSEDGFYLSFAEALR
AHSCLSDRILQYSRIVGGWDLLPRALLSSLSGLVLLNAPVVAMTQGPHDVHVQIETSPARNL
KVLKADVVLITASGPRAVKRITFSPPLPRHMQEALRRLHYVPATKVFLSFRRPFWREEHIEGG
HSNTDRPSRMIFYPPPREGALLLASYTWSAAAAFAGLSREEALRLALDDVAALHPVVRQL
WDGTGVVKRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIYFAGEHTAYPHGWETAVKS
ALRAAIKINSRKGPASDTASPEGHASDMEGQGHVHGVAASSPSHDLAKEEGSHPPVQGQLSLQ
NTTHTRTSH

Signal peptide:

amino acids 1-21

FIGURE 51

CTGACATGGCCTGACTCGGGACAGCTCAGAGCAGGGCAGAACTGGGGACACTCTGGGCCGCCTTCTGCCTGC**AT**
GGACGCTCTGAAGCCACCCGTCTGGAGGAACCACGAGCGAGGGAAAGAAGGACAGGGACTCGTGTGGCAGGAA
 GAACTCAGAGCCGGGAAGCCCCATTCACTAGAACGACTGAGAGATGCGGCCCTCGCAGGGCTGAAATTTCCT
 GCTGCTGTTACAAGATGCTTTATCTTAACCTTTGTTCCCCACTTCGACCCGGCGTTGATCTGCAT
 CCTGACATTTGGAGCTGCCATCTTCTTGTGGCTGATCACAGACCTCAACCCGCTTACCTCTTGACCTGAA
 CAATCAGTCTGTGGGAATTGAGGGAGGAGCACCGAAGGGGTTCCAGAAGAACAAATGACCTAACAGTTGCTG
 CTTCTCAGATGCCAAGAACATGTATGAGGTTTCCAAGAGGACTCGCTGTGACAAATGGGCCCTGCTGG
 ATATAGAAAACCAAACCGCCCTACAGATGGCTATCTAACAAACAGGTGCTGATAGAGCAGAGTACCTGGGTT
 CTGTCCTGATCAAAGGTATAAATCATCACAGACCGATTGTCGGCATCTTGCTCAGAATAGGCCAGAGTG
 GATCATCTCGAATTGGCTGTTACACGTACTCTATGGTAGCTGTACCTCTGATGACACCTTGGGACCAGAAC
 CATCGTACATATTGTCACAAAGGCTGATATGCCATGGTGTGACACACCCAAAAGGCATTGGTGTGAT
 AGGAATGTAGAGAAAGGCTTCACCCCGAGCCTGAAGGTGATCATCCTTATGGACCCCTTGATGATGACCTGAA
 GCAAAGAGGGAGAAGAGTGAATTGAGATCTTATCCCTATATGATGCTGAGAACCTAGGAAAGAGCACTTCAG
 AAAACCTGTGCCCTCTAGCCCAGAAGACCTGAGCTCATCTGCTTACCCAGTGGGACCACAGGTGACCCAAAGG
 AGCCATGATAACCCATCAAATATTGTTCAAATGCTGCGCTTCTCAAATGTGTGGAGCATGCTTATGAGCC
 CACTCCTGATGATGTGGCCATATCCTACCTCCCTGGCTCATATGTTGAGAGGATTGTACAGGCTTGTGTA
 CAGCTGTGGAGGCCAGAGTTGGATTCTCCAAGGGGATATTGGTTGCTGGCTGACGACATGAAGACTTGAAGCC
 CACATTGTTCCCGCGGTGCGCTGACTCTAACAGGATCTACGATAAGGTACAAATGAGGCCAGACACCCCT
 GAAGAAGTTCTTGTGAAGCTGGCTTCCAGTAAATTCAAAGAGCTTCAAAGGGTATCATCAGGCATGATAG
 TTTCTGGGACAAGCTCATCTTGCAAAGATCCAGGACAGCCTGGCGGAAGGGTCTGTAATTGTCAGTGGAGC
 TGCCCCCATGTCCACTTCAGTCATGACATTCTCCGGCAGCAATGGGATGTCAGGTGTATGAAGCTTATGGTCA
 AACAGAATGCAAGGTGGCTGTACATTACATTACCTGGGACTGGACATCAGTCACGTGGGTGCCCTGGC
 TTGCAATTACGTGAAGCTGGAGATGTGGCTGACATGAACTACTTACAGTGAATAATGAAGGAGAGGTCTGCAT
 CAAGGGTACAAACGTGTCAAAGGATACTGAGGACACAGGAAGGCCCTGGACAGTGTGGCTG
 GCTTCACACAGGAGACATTGGTCGCTGGCTCCGAATGGAACACTCTGAAAGATCATGACCCGTAAAAAGAACATT
 CAAGCTGGCCAAGGAGAATACATTGCAACCAGAGAAGATAGAAAATATCTACACACAGGAGTCACCGTGTACA
 AATTGGTACACGGGAGAGCTTACGGTCATCCTTAGTAGGAGTGGTTCTGACACAGATGTAATTCCCTC
 ATTGCAAGCCAAGCTTGGGTGAAGGGCTCTTGAGGAAGTGGCTTAAACATTGAAACAGGCAAAGCATTTCATCC
 AGAGCCATTTCATTGAAAATGGCTCTTGACACCAAACATTGAAAGCAAAGCGAGGAGAGCTTCAAATACTT
 TCGGACCCAAATTGACAGCCTGTATGAGCACATCCAGGAT**TAGGATAAGGTACTTAAGTACCTGCCGCCACTG**
 TGCACGTGTTGTGAGAAAATGGATAAAAATCTTACATTGTTGCTTCTCTCTTAAACCTTAAACC
 TGTAAACTCTAAAGCCATAGCTTTGTTATATTGAGACATATAATGTGAAACTTAGTCCCAAATAATCA
 ATCTGTCCTTCCCATTGATGTTGCTAATATTAAGGCTTCAGGGCTACTTTATCAACATGCCTGTCTCAA
 GATCCCAGTTATGTTCTGTGTCCTCCTCATGATTCAAACCTTAATACTATTAGTAACCACAAGTCAAGGGT
 CAAAGGGACCCCTGTGCCCTCTTGTGATAAACATAACTGCCAACAGTCTATGCTTATTACA
 TCTCTACTGTCAAACTAAGAGATTAAATTGAAAGACTGCTTACAATTGTTCTAGCCACTCCAC
 AAACCACTAAATTTAGTTAGCCTATCACTCATGTCAATCATATCTATGAGACAAATGTCCTCGATGCTCTT
 CTGCGTAAATTAAATTGTTGACTGAAGGGAAAAGTTGATCATACCAAACATTCCCTAAACTCTAGTTAGATA
 TCTGACTTGGGAGTATTAAAATTGGGCTATGACATACTGTCCAAAGGAATGCTGTTCTAAAGCATTATT
 CAGTAGGAACGGGGAGTAAATGTTCCCTACAGTTGCTGAGCTGGAAGCTGTTGGGGAGAGGTGACA
 GGTGGGCCAGTGAACCTTCCAGTAAATGAAGCAAGCAACTGAATAAAAACCTCCTGAACTGGGAACAAAGATCT
 ACAGGCAAGCAAGATGCCACACAAACAGGCTTATTCTGTGAAGGAACCAACTGATCTCCCCCACCTGGATT
 AGAGTTCTGCTCTACCTTACCCACAGATAACACATGTTGTTCTACTTGTAATGTAAAGTCTTAAAATAAC
 TATTACAGATAAAAAAA

FIGURE 52

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60775
<subunit 1 of 1, 739 aa, 1 stop
<MW: 82263, pI: 7.55, NX(S/T): 3
MDALKPPCLWRNHERGKKDRDSCGRKNSEPGSPHSLEALRDAAPSQGLNFLLLFTKMLFIFN
FLFSPLPTPALICILTFGAAIFLWLITRPQPVLPLLDLNNSQVGIEGGARKGVSQKNNDLTS
CCFSDAKTMYEVFQRGLAVSDNGPCLGYRKPNQPYRWLSYKQVSDRAEYLGSCLLHKGYKSS
PDQFVGIFAQNRPWEIISELACYTYSMVAVPLYDTLGPEAIVHIVNKADIAMVICDTPQKAL
VLIGNVEKGFTPSSLKVIILMDPFDDDLKQRGEKSGIEILSLYDAENLGKEHFRKPVPPSPED
LSVICFTSGTTGDPKGAMITHQNIVSAAAFLKCVEHAYEPTPDVAISYLPALAHMFERIVQ
AVVYSCGARVGFFQGDIRLLADDMKTTLKPTLFPAPRLLNRIYDKVQNEAKTPLKKFLLKLA
VSSKFKELOKGIIRHDSFWDKLIFAKIQDSLGGRVRVIVTGAAPMSTSVMFFRAAMGCQVY
EAYGQTECTGGCTFTLPGDWTSGHGVVPLACNYVKLEDVADMNYFTVNNEGEVCIKGTNVFK
GYLKDPKETQEALDSDGWLHTGDIGRWPNGTLKIIDRKKNIFKLAQGEYIAPEKIEINIYNR
SQPVQLQIFVHGESLRSSLGVVVVPDTDVLPSFAAKLGVKGSFEELCQNQVVREAILEDLQKI
GKESGLKTFEQVKAIFLHPEPFSIENGLLPTLAKRGELSKYFRTQIDSILYEHIQD
```

Important features:**Type II transmembrane domain:**

amino acids 61-80

Putative AMP-binding domain signature.

amino acids 314-325

N-glycosylation site.

amino acids 102-105, 588-591 and 619-622

FIGURE 53

GGAGGC GGAGGCC CGCGC GAGCCGGCC GAGCAGT GAGGGCCCT AGCGGGGCC GAGCGGGG
 CCCGGGGCCC TAAGCC ATT CCTGAAGTCATGGGCTGGCAGGACATTGGTGACCCGCAAT
 CCGGT **ATG** GACGACTGGAAGGCCAGCCCCCATCAAGCCCTTGGGCTCGGAAGAACGG
 AGCTGGTACCTTACCTGGAAGTATAAACTGACAAACCAGCAGGGCCCTGCAGGAGATTCTGTCA
 GACAGGGGCCGTGCTTCTGCTGGACTGTCATTGTCATAATCAAGTGTGATCCTGGACA
 CTCGGCGAGCCATCAGTGAAGCCAATGAAGACCCAGAGCCAGAGCAAGACTATGATGAGGCC
 CTAGGCCGCTGGAGCCCCACGGCGAGAGGAGTGGTCCCAGGGTCTGGACGTAGA
 GGTGTATTCAAGTCGCAGCAAAGTATATGTGGAGTGGATGGCACCACTGGTGTGGAGGATG
 AGGCCCGGGAGCAGGGCCGGGCATCCATGTCATTGTCCTCAACCAGGCCACGGCACGTG
 ATGGCAAAACGTGTGTTGACACGTACTCACCTCATGAGGATGAGGCCATGGTGTATTCT
 CAACATGGTAGCGCCCGGCCAGTGCTCATCTGCACTGTCAAGGATGAGGCCCTTCCACC
 TCAAGGACACAGCCAAGGCTGCTGAGGAGCCTGGCAGCCAGGCTGGCCCTGCCCTGGC
 TGGAGGGACACATGGGCCTTCGTGGAGCAGAAAGGAGGAGTCCTGCTGAAGACAGATGTGCCATTGA
 GCTCAGCAGAACAGGAGTGGCACTGGCAGACACAGAGCTGAACCGTCGCCGCCGGCGC
 TTCTGCAGCAAAGTTGAGGGCTATGGAAGTGTATGCAAGGACCCACACCCATCGA
 GTTCAGCCCTGACCCACTCCCAGACAACAAGGTCTCAATGTGCTGTGGCTGTCAATTGCA
 GGAACCGACCCAATTACCTGTACAGGATGCTGCGCTCTGCTTCAGCCAGGGGTGTCT
 CCTCAGATGATAAACAGTTTCTTGCAGGGCTACTATGAGGAACCCATGGATGTGGTGGCACT
 GTTGAGTCTGAGGGCATCCAGCATACTCCCCTCAGCATCAAGAATGCCCGGTGTCAGC
 ACTACAAGGCCAGCCTCACTGCCACTTCAACCTGTTCCGGAGGCCAAGTTGCTGTGGTT
 CTGGAAGAGGACCTGGACATTGCTGAGTGGATTTTCAGTTCTGAGGCCAATCCATCCACCT
 ACTGGAGGAGGATGACAGCCTGTACTGCACTCTGCCTGGAATGACCAGGGTATGAACACA
 CGGCTGAGGACCCAGCACTACTGTACCGTGTGGAGACCATGCCTGGCTGGCTGGGTGCTC
 AGGAGGTCTGTACAAGGAGGAGCTGAGCCAAGTGGCCTACACCGGAAAAGCTCTGGGA
 TTGGGACATGTGGATGCGGATGCCTGAACAAACGCCGGGCCAGAGTGCACTCATCCCTGACG
 TTTCCGATCCTACCACTTGGCATCGTCGGCTCAACATGAATGGCTACTTCAAGGAGGCC
 TACTTCAGAACAGCAAGTCAACACGGTCCAGGTGTCAGCTCAGGAATGTGGACAGTCT
 GAAGAAAGAAGCTTATGAAGTGGAGTTCACAGGCTGCTCAGTGAGGCTGAGGTTCTGGACC
 ACAGCAAGAACCCCTGTGAAGACTCTTCTGCCAGACACAGAGGGCCACACCTACGTGGCC
 TTTATTGCAATGGAGAAAGATGATGACTTCACCACTGGACCCAGCTGCCAAGTGCCTCCA
 TATCTGGGACCTGGATGTGCGTGGCAACCATGGGGCTGTGGAGATTGTTCGGAAGAAGA
 ACCACTTCTGGTGGTGGGGTCCGGCTTCCCCCTACTCAGTGAGAACGCCACCCCTCAGTC
 ACCCCAATTTCCTGGAGCCACCCCAAAGGAGGAGGGAGCCCCAGGAGCCCAGAACAGAC
A**TG****A** GACCTCCCTCAGGACCCCTGCGGGCTGGTACTGTGTACCCCAAGGCTGGCTAGCCCT
 TCCCTCCATCCTGTAGGATTTGTAGATGCTGGTAGGGCTGGGCTACCTTGTGTTAAC
 TGAGACTTAATTACTCAAGGGAGGGTCCCTGCTCAACACCCGTTGAGT
 AAAAGTCTATTATTACTTCCTGTTGGAGAAGGGCAGGAGAGTACCTGGGAATCATTACG
 ATCCCTAGCAGCTCATCCTGCCCTTGAATACCCCTACCTTCAGGCCTGGCTCAGAACATCTA
 ACCTATTATTGACTGTCTGAGGGCCTTGAAGAACAGGCCAGCTGGAGGGCTGGATTT
 TTTTGGGCTGGAATGCTGCCCTGAGGGTGGGCTGGCTTACTCAGGAAACTGCTGTGCC
 CAACCCATGGACAGGCCAGCTGGGCCACATGCTGACACAGACTCACTCAGAGACCCTA
 GACACTGGACCAGGCCTCCTCAGCCTCTTGTCCAGATTCCAAAGCTGGATAAGTT
 GGTCAATTGATTAAAAAAGGAGAAGCCCTGGGAAAAAAAAAAAAAAA

FIGURE 54

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA61185
><subunit 1 of 1, 660 aa, 1 stop
><MW: 75220, pI: 6.76, NX(S/T): 0
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REQGRGIHVIVLNQATGHVMAKRVFDTYSPEDEAMVLFLNMVAPGRVLICTVKDEGSFHLK
DTAKALLRSLGSQAGPALGWRDTWAFVGRKGGPVFGEKHSKSPALSSWGDVLLKTDVPLSS
AEEAECHWADTELNRLLLLFCSKVEGYGSVCSCDKDPTPIEFSPDPLPDNKVLNVPVAVIAGN
RPNYLYRMLRSLLSAQGVSPQMITYFIDGYYEEPMDVVALFGLRGIQHTPISIKNARVSQHY
KASLTATFNLFPKEAKFAVVLEEDLDIAVDFFSFLSQSIHLLEEDDSLYCISAWNDQGYEHTA
EDPALLYRVETMPGLGVLRRLSLYKEELEPKWPTPEKLWDWDMWMRMPEQRRGRECIIPDVS
RSYHFGIVGLNMNGYFHEAYFKKHKFNTVPGVQLRNDSLKEAYEVHRLLSEAEVLDHS
KNPCEDSFLPDTEGHTYVAFIRMEKDDDFTTWTQLAKCLHIWDLVRGNHRGLWRLFRKKNH
FLVVGVPASPYSVKKPPSVTPIFLEPPPKEEGAPGAPEQT

```

Important features of the protein:

Transmembrane domain:

amino acids 38-55

Homologous region to Mouse GNT1

amino acids 229-660

FIGURE 55

CGGACGCGTGGCTGGTGGAAAGGCCTAAAGAACGTGGAAAGCCCACCTCTCTTGGAACCCACAC
 CTGTTAAAGAACCTAACGCCATTAAAGCCACTGGAAATTGTTGCTAGTGGTGTGGTGAATA
 AAGGAGGGCAGA**ATGG**GATTTCATCTCATTAGCCTGCTGTCTGGCTATGTTGGTGGGATGTTA
 CGTGGCCGGAATCATTCCCTGGCTGTTAATTCTCAGAGGAACGACTGAAGCTGGTACTGTTGG
 GTGCTGGCCTCTGTGGAACTGCTCTGGCAGTCATCGTGCCTGAAGGAGTACATGCCCTTATGAA
 GATATTCTGAGGGAAAACACCACCAAGCAAGTGAACACACATAATGTGATTGCATCAGACAAAGCAGC
 AGAAAAATCAGTTGTCATGAACATGAGCACAGCCACGACCACACAGCTGCATGCCATATTGGT
 TTTCCCTCGTTCTGGCTCGTTCATGTTGCTGGACCAGATTGTAACCTCCATGTGCATTCT
 ACTGACGATCCAGAACGAGCAAGGTCTAGCAATTCCAAAATCACCACACAGCTGGTGTCCA
 TGCTGCAGCTGATGGTGTGCTTGGGAGCAGCAGCATCTACTTCACAGACAGTGTCCAGTTAATTG
 TGTTTGTGGCAATCATGCTACATAAGGCACCAGCTGCTTTGACTGGTTCTTGTGATGCATGCT
 GGCTTAGAGCGGAATCGAACATCAGAAAGCAATTGCTGGTCTTGCATTGGCAGCACCAGTTATGTCCAT
 GGTGACATACTTAGGACTGAGTAAGAGCAGTAAAGAACGCCCTTCAGAGGTGAACGCCACGGGAGTGG
 CCATGCTTTCTGCCCCGACATTCTTATGTCACAGTACATGTCCTCCCTGAGGTGGCGGA
 ATAGGGCACAGCCACAAGCCGATGCCACGGGAGGGAGAGGCCTCAGCCGCTGGAAAGTGGCAGCCCT
 GGTTCTGGGTGCCTCATCCCTCATCCTGTCAGTAGGACACCAGCATTAAATGTTCAAGGTCCAGC
 CTTGGTCCAGGGCCGTTGCCATCCAGTGAGAACAGCCGGCACGTGACAGCTACTCACTCCCTCAGTC
 TCTGTCTCACCTGCGCATCTACATGTATTCTAGAGTCAGAGGGGAGGTGAGGTTAAAACCTG
 AGTAATGGAAAAGCTTTAGAGTAGAAACACATTACGTTGAGCTAGCTATAGACATCCATTGTGT
 TATCTTTAAAAGGCCATTGACATTGCGTTAATATTCTCTTAACCTATTCTCAGGGAAAGATG
 GAATTAGTTAAGGAAAAGAGGAGAACCTCATACTCACAATGAAATAGTATTGAAATACAGT
 GTTCTGTAATTAAGCTATGCTCTTCTTAGTTAGAGGCTCTGCTACTTTATCCATTGATTGTTT
 AACATGGTCCCACATGTAAGACTGGTGTCTTAGCATCTATGCCACATGCGTTGATGGAAGGTCTA
 GCACCCACTCACTTAGATGCTAAAGGTGATTCTAGTTAATCTGGGATTAGGGTCAGGAAAATGATAGC
 AAGACACATTGAAAGCTCTTTACTCAAAAGAGATACTTAAAGGGATGTCAGAGGGATT
 TAAACAGCTCCTTGGCACGTGCCCTCTGAATCCAGCCTGCCATTCCATCAAATGGAGCAGGAGG
 TGGGAGGAGCTCTAAAGAGGTGACTGGTATTGTTAGCATTCTGTCAAGTCTCCTTGCAGAAT
 ACCTGTCCTCACATTCTAGAGAGGAGCCAAGTTCTAGTAGTTCTAGGCTTCTCAAGAA
 CAGTCAGATCACAAAGTGTCTTGGAAATTAAAGGGATATTAAATTAAAGTGTGATTGGATGGTTAT
 TGATATCTTGTAGTAGCTTTTAAAGACTACAAAATGTATGGTGTGCTTTTTTTGTTTT
 TTTTTTTAATTATTCTCTTAGCAGATCAGCAATCCCTCTAGGGACCTAAATACTAGGTCTAGCTT
 GGCAGACTGTGCTCTCACATAACCACCTGTAGCAAGATGGATCATAATGAGAAGTGTGCTA
 TTGATTAAAGCTTATGGAATCATGTCCTGCTCTCGTCTTGTCTTCTAACTTT
 TCCCTCTAGCCTCTCCTGCCACAATTGCTGCTACTGCTGGTGTAAATTGTTGTTGGGATGAATT
 CTTATCAGGACAACCCTCTGAACTGTAATAATGAAGATAATAATCTTATTCTTATCCCCTT
 CAAAGAAATTACCTTGTGTCATGCCGCTTGTGAGGCCCTAAATACCACCTCTCATGTGAA
 ATTGACACAATCACTAATCTGGTAATTAAACAATTGAGATAGCAAAAGTGTAAACAGACTAGGATA
 ATTTTTTTCATATTGCCAAAATTGTTGAAACCCCTGTCTGTCAAATAAGTGTATAATTGTAT
 TATAATTATTCTACTTCTATACCATTTCAAACACATTACACTAAGGGGGAACCAAGACTAGTT
 TCTTCAGGGCAGTGGGACGTAGTAGTTGTAAGGTTCTATGACGCCATAAGCTAGCATGCCTATG
 ATTATTTCTTCATGAATTGTCAGGGATCAGCAGCTGGAAATAAGCTGTGAGGCCCTGT
 GGCCACAGTGAGGAAAGTAGCACAATAGGATACAGTTGTTAGTCATTGGCAACAATTGCATACA
 ATTTTACTACCAAGAGAAGGTATAGTATGGAAAGTCCAAATGACTTCCTGATTGGATGTTAACAGCT
 GACTGGTGTGAGACTTGAGGTTCATCTAGTCCTTAAACTATATGGTTGCCTAGATTCTCTGGA
 AACTGACTTGTCAAATAAATAGCAGATTGAGTGTCAAAAAAAA

FIGURE 56

MDDFISISLLSLAMILVGCYVAGIIPLAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHAL
YEDILEGKHHQASETHNVIASDKAAEKSVVHEHEHSHDHTQLHAYIGVSLVLGFVFMLLVVDQ
IGNSHVHSTDDPEAARSSNSKITTLGLVVHAAADGVALGAAASTSQTSQLIVFVAIMLHK
APAAFGLVSFLMHAGLERNRIRKHLLVFALAAPVMSMVTYLGLSKSSKEALSEVNATGVAML
FSAGTFLYVATVHVLPEVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIPLILSVGHQH

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 37-56, 106-122, 211-230, 240-260, 288-304

FIGURE 57

GCTCGAGGCCGGCGCGGGAGAGCGACCCGGCGGCCTCGTAGCGGGCCCCGGATCCC
CGAGTGGCGGCCGGAGCCTCGAAAAGAGATTCTCAGCGCTGATTGAGATGATGGGCTTGG
GAAACGGCGTCGCAGCATGAAGTCGCCGCCCTCGTGCCTGGCCCTGGTGGCCTGCATC
ATCGTCTTGGGCTTCAACTACTGGATTGCGAGCTCCCGAGCGTGGACCTCCAGACACGGAT
CATGGAGCTGGAAGGCAGGGTCCGCAGGGCGGCTGCAGAGAGAGGGGCCGTGGAGCTGAAGA
AGAACGAGTTCCAGGGAGAGCTGGAGAACAGCAGCGGAGCAGCTTGACAAAATCCAGTCCAGC
CACAACTTCCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGGCCTTGGTCAA
TAACATCACCACAGGTGAGAGGCTCATCCGAGTGCTGCAAGACCAGTTAAAGACCCTGCAGA
GGAATTACGGCAGGCTGCAGCAGGATGTCCTCAGTTCAAGAACACCAGAACCTGGAG
AGGAAGTTCTCCTACGACCTGAGCCAGTGCATCAATCAGATGAAGGAGGTGAAGGAACAGTG
TGAGGGAGCGAATAGAACAGGTCACCAAAAGGGAAATGAAGCTGTAGCTTCCAGAGACCTGA
GTGAAAACAACGACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCCAGGCTGCAG
GCAGCAGGCCTGCCACACACAGAGGTGCCACAAGGGAAACGTGCTGGTAACAGCAA
GTCCCAGACACCAGCCCCAGTCCGAAGTGGTTGGATTCAAAGAGACAGTTGAGAAAG
AGGAAACCAATGAGATCCAGGTGGTGAATGAGGAGCCTCAGAGGGACAGGCTGCCAGGAG
CCAGGCCGGAGCAGGTGGAAGACAGACCTGTAGGTGGAAGAGGCTTGGGGAGCCGG
AGAACTGGGCCAGACCCACAGGTGCAGGCTGCCCTGTCAGTGAGCCAGGAAAATCCAGAGA
TGGAGGGCCCTGAGCGAGACCAGCTTGTCACTCCCGACGGACAGGAGGAGCAGGAAGCT
GCCGGGAAGGGAGAAACCAGCAGAAACTGAGAGGAGAAGATGACTACAAACATGGATGAAAA
TGAAGCAGAATCTGAGACAGACAAGCAAGCAGCCCTGGCAGGGAAATGACAGAAACATAGATG
TTTTAATGTTGAAGATCAGAAAAGAGACACCATAAATTACTTGATCAGCGTGAAAAGCGG
AATCATAACACTTGAATTGAACTGGAATCACATATTCACAACAGGGCCGAAGAGATGACTA
TAAAATGTTCATGAGGGACTGAATACTGAAAATGTACTAAATAATGTACATCTGA

FIGURE 58

MMGLGNRGRSMKSPPLVLAALVACIIVLGFNYWIASSRSVDLQTRIMELEGRVRRAAERGA
VELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQDQL
KTLQRNYGRLQQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVA
SRDLSENNNDQRQQLQALSEPQPRLQAAGLPHTEVPGKGNVLGNSKSQT PAPSSEVVLDSKR
QVEKEETNEIQVVNEEPQRDRLPQE PGREQVVEDRPVGGRGF GGAGELGQT PQVQAALSVSQ
ENPEMEGPERDQLVIPDGQEEEQEAAGEGRNQQKLRGEDDYNMDENEAESETDKQAALAGND
RNIDVFNVEDQKRDTINLLDQREKRNH TL

Signal peptide:

amino acids 1-29

FIGURE 59

GGATGCAGAAAGCCTCAGTGTGCTTCCTGGCCTGGGTCTGCTTCCTCTTCTACGCTGGCATTGCCCTTTCA
 CCAGTGGCTTCCTGCTCACCGTTGGAGCTACCAACCATAAGCAGTCCAAGAGCCCCCAGGCCCTGGTCCC
 TGCCATGGGGAGCCAAGGGAAACCTGGGCCTGCTGGATGGCTCCGATTTCGCGGGGTGTGGTGCTGA
 TAGATGCTCTGCGATTGACTTCGCCAGCCCCAGCATTACACGTGCTAGAGAGGCCTCTGTCTCCCTACCC
 TCCTGGGCAAACTAAGCTCCTTGAGAGGATCCTGGAGATTCAAGGCCACCAGGCCCTACGCTACTGCC
 TTGACCCCTCCTACCACCACCATGAGCCTCAAGGCCCTCACCAGTGGCTACTGCCAACCTTATTGATGCTG
 GTAGTAACCTGCCAGGCCAGCAGCATTAGTGAAGACAATCTCATTAAGCAGTCAACAGTGAGGAAGGGGTG
 TCTCATGGGAGATGATACTGGAAAGACCTTTCCCTGGTCTTCTCAAAGCCTTCTCCCATCCTCA
 ATGTCAGAGACCTAGACACAGTGGACAATGGCATTCTGGAAACACCTCTACCCACCAGGCCCTACCC
 ACAGTGTGATTGCTACTTCCTGGGTGGGACACTGTGGCCAAAGCATGCCCTACCCACCCTGAAATGGCA
 AGAAACTTAGGAGATGGCAGGTGATCAGGGACTTGTGGAGCGTCTGGAGAAATGACACACTGCTGGTAGTGG
 CTGGGACCATGGGATGACCAAAATGGAGACCATGGAGGGACAGTGAGCTGGAGGTCTCAGCTGCTCTTC
 TGTATAGCCCACAGCAGTCTCCAGCACCCACCAGAGGAGCCAGAGGTGATTCCTCAAGTTAGCCTGTG
 CCACGCTGCCCTGCTGGGCTGCCATCCATTGGGAAATATGGGAAAGTGTGAGCTGGTAGCTATTCTCAG
 GGGTGGAGACTCCCAGCCCCACTCCTCTGCTTAGGCCAACGCTCAGCTCATCTCAATGCTCAGCAGGTG
 CCCATTCTCATACCTACTCAGCTGCTACTCAGGACCTCAAGCTAAGGAGCTCATCAGCTGAGAACCTCT
 TCTCAAGGCTCTGCTGACTACCAAGTGGCTCTCCAGAGCCCCAACGGGGCTGAGGCAGACTGCCACTGTGA
 TTGCTGAGCTGAGCAGTCTGCCAGGGGAGCTCGGGCATGTGCATCGAGTCTGGCTCGTTCTCTGGTCC
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 CAGGCTTCCATTGCCCTACTCCTGACACCTGTGGCTGGGCTGGTGGGCACTAGCGTATGCTGGAC
 TCCTGGGAACTATTGAGCTGAAGCTAGATCTAGTGTCTAGGGCTGTGGCTGCAGTGAAGCTATTCTCC
 TTCTGTGGAAAGCCTGGCTGGCTGGGCTCAAGAGGCCCTGGCAACCCTGTTCCATCCCTGGCCGTCC
 TGTACTCCTGCTGTTGCTGGCTGTCTCTGATAGTTGTTGAGCTGAGGCCAGGGCACCCCC
 TCCTTGGGCTATTCTGCTCCTGGTGTCCAGCTCACTGGAGGGCAGCTGCTTCCACCTAACGCTAC
 TCACAATGCCCGCCCTGGCACTTCAGCCACAACAAACCCCCACGGCACAATGGTCATATGCCCTGAGGCTTG
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 CCTCTCCCTGGCTGAGCTCTGCCATGGTGGGTGGTCAGGCAAAAGATTATGGTATGGAGCTGTGTGG
 CGCGCTGGGCCCTGTTAGCTGCCGTGGCTGGCTGGGCCCTATGGTAACTCAAGAGGCCAGGCC
 CCATGCTTTGTGCGCTGGGACTGCCCTAATGGCATGGTACTGCTGCTACTGGCATTGGCGTCGGGG
 CAGATGAGGCTCCCCCGCTCTGGGCTCTGGTCTCTGGGATCCATGGTGCCTGGCTGTAGCAGGG
 TGGCTGCTTCAGGGCTCGCGCTGCTGCTGGAAAGCTGTGACAGTGTGGTAAGGCTGGGCAGGCC
 GGACAGGACTGCTCTACTCCCTCTCAGGCCCCCCTACTCTCAAGCTGACTGGATTATGTTCCCTCAA
 TCTACCGACACATGCAGGAGTTGGGGCGGTTAGAGAGGACAAATCTCAGGGTCCCTGACTGTGGCTG
 CTTATCAGTTGGGAGTGTCTACTCAGCTGCTATGGTACAGCCCTACCCCTGTTGGCCTCCACTCTGCTG
 TGATGCGGAGOGCATCAGCTGTTCTGCTGCTGGAGCTTCTCTGAGAGCTTCTCTACATCTGCTTG
 CTGGGATACCGTCACCACCCCTGGCTCTTACTGTGCCATGGCAGGCAGTCTGGCTGGGCCATGGCA
 CACAGACCTCTACTCCACAGGCCACCAGCCTGCTTCCAGCCATTGGCATGCAGCTCGTGGGATTCC
 CAGAGGGCATGGCTCTGACTGGCTGCCCTGCTTGTAGTGGAGCCAACACCTTGCCCTCCACCTCT
 TTGCGTAGGGTGGCCACTGCTCCTGCTGGCCTTCTGTGTGAGAGTCAGGGCTGGAAAGAGACAGCAG
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 ATGCCCTCAGCACTCTATGCAGCACTGCTGAGCTGGCCTCAAGTACCTCTTATCCTGGTATTCAGATT
 TGGCCTGTGCTTGGCAGCCTCCATCCTCGCAGGCATCTCATGGTCTGGAAAGTGTGCCCCCTAAGTT
 TTGAGGCTGGGCTTCATTGTGAGCAGCGTGGACTTCTCCTGGGATAGCTTGTGATGAGAGTGGATGG
 CTGTGAGCTCTGGTCAGGCTATTCTGGCCAGCAGAGGTACTGGATGCTGCAAGACAGGCC
 ACAGAGAGTGTGGAGAAACAGTGTAGCCTGGCCTGTACAGGTACTGGATGATCTGCAAGACAGGCC
 TCTTACTATCATGCAGCCAGGGGCCGTGACATCTAGGACTTCATTATTCTATAATTCTAGGAC
 ACAGGAGCAGTGGAGTAAATGGCCGGTCTCCGAAGTGGAAATAAAATAGGCC
 TGATCCCTAACTCCTGATTGGATGATCTGAGGGACAAGGGGGCGGTCTCCGAAGTGGAAATAAA
 AGGCCGGCGTGGTAGCTGCACCTATAATCCAGCACTTGGGAGGGCAGAGGTGGAGGATTGCTTGG
 CTGGTCCCAGGAGTTCAAGACCAGCTGTTAAAAAAAGTGTAAATAAAATGATAATAT

FIGURE 60

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809
<subunit 1 of 1, 1089 aa, 1 stop
<MW: 118699, pI: 8.49, NX(S/T): 2
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MASRFSRVVLVLIDALRFDAQPQHSHVPREPPVSLPFLGKLSSLQRILEIQPHHARLYRSQ
VDPPTTMQRALKALTGSLPTFIDAGSNFASHAIVEDNLIKQLTSAGRVVFMGDDTWKDLF
PGAFSKAFFFPSFNVRDLDVDNGILEHLYPTMDSGEWDVLIAHFLGVDHCGKHGPHEM
AKKLSQMDQVIQGLVERLENDTLLVVAGDHGMTTNGDHGGDSELEVSAALFLYSPTAVFPST
PPEEPEVIPQSVLVPTLALLGLPIPFGNIGEVMAELFSGGEDSQPHSSALAQASALHLNAQ
QVSRLFHTYSAATQDLQAKELHQLQNLFSKASADYQWLLQSPKGAEATLPTVIAELQQFLRG
ARAMCIESWARFSLVRMAGGTALLAASCFCICLILASQWAISPGFPFCPLLLTPVAWGLVGAIA
YAGLLGTIELKLDLVLLGAVAAYSSFLPFLWKAWAGWGSKRPLATLFPIPGPVLLLLFRLA
VFFSDSFVVAEARATPFLLGSFILLVVQLHWEGQLLPPKLLTMPRLGTSATTNPPRHNGAY
ALRLGIGLLLCTRLLAGLFHRCPEETPVCHSSPWLSPLASMVGGRAKNLWYGACVAALVALLA
AVRLWLRRYGNLKSPEPPMLFVRWGLPLMALGTAAYWALASGADEAPPRLRLVSGASMVLP
RAVAGLAASGLALLWKPVTVLVKAGAGAPRTRTLTPFGPPTSQADLDYVVPQIYRHMQE
EFRGRLERTKSQGPLTVAAAYQLGSVYSAAMVTALTLLAFPLLLLHAERISLVFLLLFLQSFL
LLHLLAAGIPVTPGPFTVPWQAVSAWALMATQTFYSTGHQPVFPAIHWHAAFVGFPEGHGS
CTWLPALLVGANTFASHLLFAVGCPLLLWPFLCESQGLRKRQQPPGNEADARVRPEEEEP
LMEMRLRDAPQHFYAALLQLGLKYLFIQILACALAASILRRHLMVWKVFAPKFIFEAVG
FIVSSVGLLLGIALVMRVDGAVSSWFRQLFLAQQR
```

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domains:amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850,
1016-1034, 1052-1070**Leucine zipper pattern.**

amino acids 843-864

N-glycosylation sites.

amino acids 37-40, 268-271

FIGURE 61

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCCCTGGGGACGGGCAGTCCCTGT
 GTCTCTGGTGGTTGCCTAAACCTGCAAACATCACTTCTTATCCATCAACATGAAGA**ATGT**
 CCTACAATGGACTCCACCAGAGGGTCTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATT
 TCATCACAAATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTCTGTTGT
 CCTGACAGCTCCAGAGAAGTGGAGAGAAATCCAGAACCTCCTGTTCCATGCAACAAA
 TATACTCCAATCTGAAGTATAACGTGCTGTGAATACTAAATCAAACAGAACGTGGTCC
 CAGTGTGTGACCAACCACACGCTGGTGTCACCTGGCTGGAGCCGAACACTCTTACTGCGT
 ACACGTGGAGTCCTCGTCCCAGGGCCCCCTGCCGTGCTCAGCCTCTGAGAAGCAGTGTG
 CCAGGACTTGAAAGATCAATCATCAGAGTTCAAGGCTAAAATCATCTCTGGTATGTTTG
 CCCATATCTATTACCGTGTTCCTTTCTGTGATGGCTATTCCATCTACCGATATATCCA
 CGTTGGCAAAGAGAAACACCCAGCAAATTGATTGATTTGAAATGAATTGACAAAAA
 GATTCTTGTGCCTGCTGAAAAAAATCGTATTAACTTATCACCCCTCAATATCTGGATGAT
 TCTAAAATTCTCATCAGGATATGAGTTACTGGAAAAAGCAGTGATGTATCCAGCCTAA
 TGATCCTCAGCCCAGCGGAAACCTGAGGCCCTCAGGAGGAAGAGGAGGTGAAACATTAG
 GGTATGCTTCGCATTGATGAAATTGGTACTCTGAAGAAAACACGGAAGGTACTTCT
 CTCACCCAGCAAGAGTCCCTCAGCAGAACAAATACCCCCGGATAAAACAGTCATTGAATATGA
 ATATGATGTCAGAACCACTGACATTGTGCGGGGCCTGAAGAGCAGGAGCTCAGTTGCAGG
 AGGAGGTGTCCACACAAGGAACATTATTGGAGTCGCAGGCAGCGTGGCAGTCTGGCCCG
 CAAACGTTACAGTACTCATACACCCCTCAGCTCCAAGACTTAGACCCCTGGCGCAGGAGCA
 CACAGACTCGGAGGAGGGCCGGAGGAAGAGCCATCGACGACCCCTGGTCAGTGGATCCCC
 AAACGGCAGGCTGTTATTCTCGCTGTCAGCTCGACCAGGATTAGAGGGCTGCGAG
 CCTTCTGAGGGGGATGGGCTCGGAGAGGAGGGCTTCTATCTAGACTCTATGAGGAGCCGGC
 TCCAGACAGGCCACCAGGAGAAAATGAAACCTATCTCATGCAATTGAGGAATGGGGGT
 TATATGTGCAGATGAAAC**TGA**TGCCAACACTCCTTGCCTTGTGCAAAC
 AAGTGAGTCACCCCTTGATCCCAGCCATAAAAGTACCTGGGATGAAAGAAGTTTCCAGT
 TTGTCAGTGTCTGTGAGAATTACTTATTCTCTATTCTCATAGCACGTGTGATTG
 GTTCATGCATGTAGGTCTCTAACATGATGGTGGCCTCTGGAGTCCAGGGCTGGCCGGT
 TGTTCTATGCAGAGAAAGCAGTCATAAAATGTTGCCAGACTGGGTGCAGAATTATTCAAGG
 TGGGTGT

FIGURE 62

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62815
<subunit 1 of 1, 442 aa, 1 stop
<MW: 49932, pI: 4.55, NX(S/T): 5
MSYNGLHQRFKELKLLTLCISISSQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQ
QIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNLTYCVHVESFVPGPPRRAQPSEKQ
CARTLKQDQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHPANLILIGNEFD
KRFFVPAEKIVINFITLNISDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEVKH
LGYASHLMEIFCDSEENTEGTSLTQQESLSRTIPPDKTVIEYEYDVRTTDICAGPEEQELSL
QEEVSTQGTLLSQAAALAVLGQTLQYSYTPQLQDLDPLAQEHTDSEEGPEEEPSTTLVDWD
PQTGRLCIPSLSSFDQDSEGCEPSEGDSLGEGLSRLYEEPAPDRPPGENETYLMQFMEEW
GLYVQMCN
```

Important features:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 140-163

N-glycosylation sites.

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

FIGURE 63

CGGACGCGTGGCGGACGCGTGGCGGACGCGTGGGTCTCTGCAGGGAGACGCCAGCCTGCG
TCTGCCATGGGGCTCGGGTTGAGGGCTGGGACGTCCCTGCTGACTGTGGCCACCGCCCT
GATGCTGCCGTGAAGCCCCCGCAGGCTCCTGGGGGCCAGATCATGGGGGCCACGAGG
TGACCCCCCACTCCAGGCCTACATGGCATCCGTGCGCTTCGGGGCCAACATCACTGCGGA
GGCTTCCTGCTGCGAGCCCCTGGGTGGTCTCGGCCGCCACTGCTCAGCCACAGAGACCT
CCGCACTGGCCTGGTGGTGCTGGCGCCACGTCTGAGTACTGCGGAGCCCACCCAGCAGG
TGTTTGGCATCGATGCTCTCACACGCACCCGACTACCACCCATGACCCACGCCAACGAC
ATCTGCCTGCTGCGCTGAACGGCTTGCTGCTGGGCCCTGCAGTGGGCTGCTGAGGCT
GCCAGGGAGAAGGGCCAGGCCCCCACAGCGGGACACGGTGCCGGTGGCTGGCTGGGCT
TCGTGTCTGACTTGAGGAGCTGCCCTGGACTGATGGAGGCCAAGGTCCGAGTGCTGGAC
CCGGACGTCTGCAACAGCTCTGGAAGGGCCACCTGACACTTACCATGCTCTGCACCCGAG
TGGGGACAGCCACAGACGGGCTTCTGCTGCCGACTCCGGAGGGCCCTGGTGTGCAGGA
ACCGGGCTCACGGCCTCGTTCTCGGGCCTCTGGTGC GGACCCCCAAGACCCCCGAC
GTGTACACGCAGGTGTCCGCCCTTGATCTGGACGTGGTTCGGCGAGCAGTCC
CCAGCCCAGGCCCCCTGCCTGGGACCAACCAGGCCAGGAGAAGGCCTGAGCCACAACCT
TGCAGGATGCAAATGAGATGCCGCTCCAGGCCTGGAATGTTCCGTGGCTGGGCCCCACGGG
AAGCCTGATGTTAGGGTTGGGTGGGACGGGAGCGGGTGGGCACACCCATTCCACATGCA
AAGGGCAGAAGCAAACCCAGTAAATGTTAACTGACAAAAAAAAAAAAAGAAA

FIGURE 64

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845
><subunit 1 of 1, 283 aa, 1 stop
><MW: 30350, pI: 9.66, NX(S/T): 2
MGLGLRGWGRPLLTVALMLPVKPPAGSWGAQIIGGHEVTPHSRPYMASVRFGGQHHCGGF
LLRARWVVSAAHCFSHRDLRTGLVVLGAHVLSTAEPQQVFGIDALTTHPDYHPMTHANDIC
LLRLNNGSAVLGPAVGLLRLPGRRARPPTAGTRCRVAGWGFVSDFEELPPGLMEAKVRVLDPD
VCNSSWKGHLTLMCTRSGDHSRRGFCSADSGGPLVCRNRAHGLVSFSGLWC GDPKT PDVY
TQVSAFVAWIWDVVRSSPQPGPLPGTTRPPGEAA
```

Signal peptide:

amino acids 1-30

FIGURE 65

GAGCTACCCAGGCGGCTGGTGTGCAGCAAGCTCGCGCCACTCCGGACGCCGTACGCCCTGA
 CGCCTGTCCCCGGCCCGGCA**ATG**AGCCGCTACCTGCTGCCGCTGTCGGCGCTGGGACCGTAG
 CAGGCGCCGCCGTGCTGCTCAAGGACTATGTCACCGGTGGGCTGCCCAAGCAAGGCCACC
 ATCCCTGGGAAGACGGTCATCGTACGGGCGCCAACACAGGCATGGGAAGCAGACCGCCTT
 GGAACCTGGCCAGGAGAGGAGGCAACATCATCCTGGCCTGCCAGACATGGAGAAGTGTGAGG
 CGGCAGCAAAGGACATCCGCCGGGAGACCCCTCAATCACCATGTCAACGCCGGCACCTGGAC
 TTGGCTTCCCTCAAGTCTATCCGAGAGTTGCAGCAAAGATCATTGAAGAGGGAGGAGCGAGT
 GGACATTCTAACAAACGCGGGTGTGATGCCGTGCCCCACTGGACCACCGAGGACGGCT
 TCGAGATGCAGTTGGCGTTAACCACCTGGTCACTTCTCTTGACAAACTTGCTGCTGGAC
 AAGCTGAAAGCCTCAGCCCCTCGCGGATCATCACCTCTCGTCCCTGCCCATTTGCTGG
 GCACATAGACTTGAACGACTTGAACGGCAGACGAGGAAGTATAACACCAAAGCCGCCTACT
 GCCAGAGCAAGCTGCCATCGTCCCTTCACCAAGGAGCTGAGCCGGCGCTGCAAGGCTCT
 GGTGTGACTGTCAACGCCCTGCACCCGGCGTGGCCAGGACAGAGCTGGCAGACACACGGG
 CATCCATGGCTCCACCTCTCAGCACACACTCGGCCCATCTTGCTGCTGGTCAAGA
 GCCCCGAGCTGGCCGCCAGCCCAGCACATACCTGGCGTGGCGAGGAAGTGGCGGATGTT
 TCCGGAAAGTACTCGATGGACTCAAACAGAAGGCCGGCCGGAGGCTGAGGATGAGGA
 GGTGGCCGGAGGCTTGGCTGAAAGTGCCGCTGGTGGCTAGAGGCTCCCTGTGA
 GGGAGCAGCCCTCCCCAGA**TAA**CCTCTGGAGCAGATTGAAAGCCAGGATGGCGCCTCAG
 ACCGAGGACAGCTGCCATGCCCGAGCTTGGACTACCTGAGCCGGAGACCCAG
 GACTGGCGGCCATGCCCGAGCTAGGTTCTAGGGCGGTGCTGCCAGTGGACTGGC
 CTGCAGGTGAGCACTGCCGGCTCTGGCTGGTCCGTGCTCTGCTGCCAGCAGGGAG
 AGGGCCATCTGATGCTTCCCTGGGAATCTAAACTGGGAATGGCGAGGAGGAAGGGGCTC
 TGTGCACTGCAGGCCACGTCAGGAGAGCCAGCGGTGCTGTCGGGAGGGTCCAAGGTGC
 TCCGTGAAGAGCATGGCAAGTTGTCTGACACTTGGTGGATTCTGGTCCCTGTGGACCT
 TGTGCATGCATGGCCTCTCTGAGCCTTGGTTCTCAGCAGTGGAGATGCTCAGAATACTG
 CTGTCTCCCATGATGGTGTGGTACAGCGAGCTGTTGCTGGCTATGGCATGGCTGTGCCGG
 GGTGTTGCTGAGGGCTTCCGTGCCAGAGCCCAGCCAGAGAGCAGGTGCAGGTGTCA
 GAGTTCAAGGCTCTGCACGGCATGGAGTGGGAACCCACCAGCTGCTGCTACAGGACCTGGGA
 TTGCCTGGACTCCCACCTCCTATCAATTCTCATGGTAGTCCAAACTGCAGACTCTCAAAC
 TTGCTCATT

FIGURE 66

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64842
><subunit 1 of 1, 331 aa, 1 stop
><MW: 35932, pI: 8.45, NX(S/T): 1
MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELARRG
GNIIILACRDMEKCEAAAKDIRGETLNHHVNARHLDLASLKSIREFAAKIIEEEERVDILINN
AGVMRCPHWTTEDGFEMQFGVNHLGHFLLTNLLDKASAPSRIINLSSLAHVAGHIDFDD
LNWQTRKYNTKAAYCQSKLAIVLFTKELSRRLQGSGVTVNALHPGVARTELGRHTGIHGSTF
SSTTLGPIFWLLVKSPELAAQPSTYLAVAEELADVSGKYFDGLKQKAPAPEAEDEEVARRLW
AESARLVGLEAPSVRQPLPR
```

Signal peptide:

amino acids 1-17

FIGURE 67

GAAGTTCGCGAGCGCTGGC**ATG**TGGTCTGGGCGCGCTGGCGCGCTGCTGGCGGTGCTG
 GCGCTCGGGACAGGGAGACCCAGAAAGGGCTGCGGCTCGGGCGACACGTTCTCGGCCTGAC
 CAGCGTGGCGCGCCCTGGCGCCCGAGCGCCGGCTGCTGGGCTGCTGAGGCGGTACCTGC
 GCAGGGAGGAGGCGCGCTGCGGACCTGACTAGATTCTACGACAAGGTACTTCATTTGCAT
 GAGGATTCAACAACCCCTGTGGCTAACCTCTGCTTGCAATTACTCTCATCAAACGCCGTGCA
 GTCTGACTGGAGGAATGTGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTGTGAAGG
 ATGGCTATGAGAAGGTGGAGCAAGACCTTCCAGCCTTGAGGACCTTGAGGGAGCAGCAAGG
 GCCCTGATGCGGCTGCAGGACGTGTACATGCTCAATGTGAAAGGCCCTGGCCCCGAGGTGTCTT
 TCAGAGAGTCACTGGCTCTGCCATCACTGACCTGTACAGCCCCAACGGCTCTTCTCA
 CAGGGGATGACTGCTCCAAGTTGGCAAGGTGGCCTATGACATGGGGATTATTACCATGCC
 ATTCCATGGCTGGAGGAGGCTGTCAGTCTTCCGAGGATCTACGGAGAGTGGAAAGACAGA
 GGATGAGGCAAGTCTAGAAGATGCCTTGGATCACTTGGCTTGTATTCCGGGCAGGAA
 ATGTTCTGTTGCCCTCAGCCTCTCGGGAGTTCTCTACAGCCCAGATAATAAGAGG
 ATGGCCAGGAATGTCTTGAATATGAAAGGCTTGGCAGAGAGCCCCAACCACGTGGTAGC
 TGAGGCTGTCACTCAGAGGCCAATATAACCCACCTGCAGACCAGAGACACCTACGAGGGGC
 TATGTCAGACCCCTGGGTTCCCAGCCACTCTACCAAGATCCCTAGCCTCTACTGTTCTAT
 GAGACCAATTCCAACGCCAACCTGCTGCTCCAGCCCACCGGAAGGGAGGTCACTCCACCTGGA
 GCCCTACATTGCTCTTACCATGACTCGTCAGTGACTCAGAGGCTCAGAAAATTAGAGAAC
 TTGCAGAACCATGGCTACAGAGGTCACTGGTGGCATCAGGGAGAACAGTTACAAGTGGAG
 TACCGCATTGCTGCCCTCACAGGCCCTGATGTCCGGCTCCCTATGCAGAGTATCTGCAGG
 TGGTGAACTATGGCATCGGAGGACACTATGAGCCTCACTTGACCATGCTACGTACCAAGC
 AGCCCCCTACAGAATGAAGTCAGGAAACCGAGTTGCAACATTATGATCTATCTGAGCTC
 GGTGGAAGCTGGAGGAGCCACAGCCTCATCTATGCCAACCTCAGCGTGCCTGTGGTTAGGA
 ATGCAGCACTGTTGGAAACCTGACAGGAGTGGTAAGGGGACAGTGACACACTTCAT
 GCTGGCTGTCCTGTCCTGGTGGAGATAAGTGGGTGGCAACAAAGTGGATACATGAGTATGG
 ACAGGAATTCCGCAGACCCCTGCAGCTCAGCCCTGAAGAC**TGA**ACTGTTGGCAGAGAGAAC
 TGGTGGAGTCCTGTGGCTTCCAGAGAACGCCAGGAGCCAAAAGCTGGGTAGGAGAGGAGAA
 AGCAGAGCAGCCTCTGGAAAGAACGCCCTGTCAGCTTGTGCCTCGCAAATCAGAGGC
 AAGGGAGAGGTTGTTACCAAGGGACACTGAGAATGTACATTGATCTGCCCAACGGAA
 GTCAGAGTAGGATGCACAGTACAAAGGAGGGGAGTGGAGGCCAGAGAGGAAGTTCTGG
 AGTTCAAGATACTCTGTTGGAAACAGGACATCTCAACAGTCTCAGGTTGATCAGTGGTC
 TTTGGCACTTGAACCTTGACCACAGGGACCAAGAACAGTGGCAATGAGGACACCTGCAGGAG
 GGGCTAGCCTGACTCCCAGAACATTAAAGACTTCTCCCCACTGCCTCTGCTGCAGCCCCAAG
 CAGGGAGTGTCCCCCTCCAGAACATATCCCAGATGAGTGGTACATTATATAAGGATTTT
 TTTAAGTTGAAAACAACATTCTTTCTTTGTATGATGGTTTTAACACAGTCATTAAAA
 ATGTTATAAAATCAAAA

FIGURE 68

MGP GARLA ALLA VLA LAL GTGD PER AARGDT FSA L TS VAR ALA PERR LLG LL RRY LRGE EARL
RDL TRFY DKV LSL HED STTP VAN PLLA FT LIKRL QSD WRN VVHS LEASE N IRALK DGY EK VE
QDL PAFED LEGA ARAL MRL QDV YML NVK GLARG VFQR VTGS AITD LYSP KRL FSL TGDD CFQ
VGKV AYDM GDYY HAI PW LEE AVS LFR GSY GEW KTE DEAS LED ALD HLA FAY FRAG NVSC ALS
LSREF LLYSPDN KRMAR NVL KYER LLA E SPN HVA E AVI QRP NI PHL QTR DT YEG LCQ TLGS
QPT LYQ I PSL YCS YET NSN AYLL QPI RKE VIH LEP YI ALY HDF VSD SE A QKIRE LAEP WL Q
RSVV ASGE KQL QVE YRIS KS A WL KDT VDP KL VTL NHRIA ALT GLD VR P P YAE YL QV NY GIG
GHYE PHFD HAT SPSS PLY RMK SGN RVAT FMI YL SS VE AGG AT AFI YAN LS VP VVR NA AL FW W
NLH RS GEG DSD TLH AGCP VL VGDK WANK WI HEY GQE FRR PCSS PED

Signal peptide:

amino acids 1-19

FIGURE 69

GAGATAGGGAGTCTGGGTTAACGTCCTGCTCCATCTCAGGAGCCCCTGCTCCCACCCCTAG
 GAAGCCACCAGACTCCACGGTGTGGGCCAATCAGGTGGAATCGGCCCTGGCAGGTGGGCC
 ACGAGCGCTGGCTGAGGGACCGAGCCGGAGAGCCCCGGAGCCCCCGTAACCCGCGCGGGAG
 CGCCCAGGATGCCGCGCGGGACTCGGAGCAGGTGCGCTACTGCGCGCGCTTCTCCTACCTC
 TGGCTCAAGTTTCACTTATCATCTATTCCACCGTGTCTGGCTGATTGGGCCCTGGTCCT
 GTCTGTGGCATCTATGCAGAGGTTGAGCGGAGAAATATAAAACCTTGAAAGTGCCTTCC
 TGGCTCCAGCCATCATCCTCATCCTGGCGTGTACGTTCTCCAAGCATTGATGTACATCCTGGAT
 CTGCCTCATCATGGAGCTCATTGGTGGCGTGGTGGCCTTGACCTTCCGGAACAGACCATTG
 ACTTCCTGAACGACAACATTGAAGAGGAATTGAGAACTACTATGATGATCTGGACTTCAA
 AACATCATGGACTTGTCAAGAAAAGTTCAAGTGCTGTGGCGGGAGGACTACCGAGATTG
 GAGCAAGAACAGTACCAACGACTGCAGTGCCCCCTGGACCCCTGGCCTGTGGGTGCCCTACA
 CCTGCTGCATCAGGAACACGACAGAACAGTTGTAACACCATGTGTGGCTACAAACTATCGAC
 AAGGAGCGTTCACTGTGCAGGATGTCATCTACGTGCGGGCTGCACCAACGCCGTGATCAT
 CTGGTCATGGACAACACTACCATCATGGCGTGCATCCTCCTGGCATTGCTTCCCCAGT
 TCCTGGGGGTGCTGCTGACGCTGCTGTACATCACCCGGTGGAGGACATCATGGAGCAC
 TCTGTCACTGATGGCTCCTGGGCCCGGTGCCAAGCCCAGCGTGGAGGCCAGGCACGGG
 ATGCTGCTTGTGCTACCCAAATGGGCCAGCCTGCCATGGCAGCTCCAACAAGGACCGTC
 TGGGATAGCACCTCTCAGTCAACATCGTGGGCTGGACAGGGCTGCCCTCTGCCACA
 CTCAGTACTGACCAAAGCCAGGGCTGTGTGCCTGTGTAGGTCCCACGGCTCTGCCTC
 CCCAGGGAGCAGAGCCTGGGCCCTCCCTAACAGAGGCTTCCCCGAGGCAGCTCTGGAATCTGT
 GCCCACCTGGGCCTGGGAACAAGGCCCTCCTTCTCCAGGCCTGGCTACAGGGAGGGA
 GAGCCTGAGGCTCTGCTCAGGGCCCATTCTCATCTGGCAGTGCCCTGGCGTGGTATTCAA
 GGCAGTTTGTAAGCACCTGTAATTGGGAGAGGGAGTGTCCATGCAGCCACGCCATGGCAGGTTGGC
 GCATCTGGGAAGGGCAGGAGGGAAAGAGCTGTCATGCCAGCCACGCCATGGCAGGTTGGC
 CTCTTCTCAGCCTCCAGGTGCCTTGAGCCCTTGTCAAGGGCGCTGCTTCTTGAGCCTA
 GTTTTTTACGTGATTTGTAAACATTCTTGTACAGATAACAGGAGTTCTGAC
 TAATCAAAGCTGGTATTCCCCGATGTCTATTCTGCCCTCCCCAACAGTTGTTAA
 TCAAACAATAAAACATGTTGTTGTTTAAAAAA

FIGURE 70

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863
><subunit 1 of 1, 294 aa, 1 stop
><MW: 33211, pI: 5.35, NX(S/T): 3
MPRGDSEQVRYCARFSYWLKFSLIIYSTVFWLIGALVLSVGIVYAEVERQKYKTLESAFLAP
AIIILILLGVVMFMVSFIGVLASLRDNLYLLQAFMYILGICLIMELIGGVVALTFRNQTIDFL
NDNIRRGHENYYDDLDFKNIMDFVQKKFKCCGGEDYRDWSKNQYHDCSAPGPLACGVPYTCC
IRNTTEVVNTMCGYKTIDKERFSVQDVIYVRGCTNAVIIWFMDNYTIMACILLGILLPQFLG
VLLTLLYITRVEDIIMEHSVTDGLLGPAGAKPSVEAAGTGCLCYPN
```

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 22-42, 57-85, 93-116, 230-257

FIGURE 71

GAGGAGCGGGCCGAGGACTCCAGCGTCCCCAGGTCTGGCATCCTGCACTTGCTGCCCTCTGA
 CACCTGGGAAGATGGCCGGCCCCTGGACCTTCACCCTCTGTGGTTGCTGGCAGCCACC
 TTGATCCAAGCCACCCCTCAGTCCCCTGCAGTTCTCATCCTCGGCCAAAAGTCATCAAAGA
 AAAGCTGACACAGGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGC
 TCAGTGCCATGCCGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGCAGCCTGGTGAACACC
 GTCCCTGAAGCACATCATCTGGCTGAAGGTATCACAGCTAACATCCTCCAGCTGCAGGTGAA
 GCCCTCGGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCA
 ACACGCCCTGGTCAAGACCATCGTGGAGTTCCACATGACGACTGAGGCCAACCCATC
 CGCATGGACACCAGTGCAAGTGGCCCCACCCGCCCTGGTCCCTCAGTGACTGTGCCACCAGCA
 TGGGAGCCTGCGCATCCAACTGCTGTATAAGCTCTCCTGGTGAACGCCCTAGCTAAC
 AGGTATGAACCTCCTAGTGCCATCCCTGCCAATCTAGTGAAAAAACAGCTGTGTCCCCTG
 ATCGAGGCTTCCTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTGAAGGTGCCATT
 CCTCAGCATTGACCGTCTGGAGTTGACCTCTGTATCCTGCCATCAAGGGTGACACCATT
 AGCTCTACCTGGGGCCAAGTTGGACTCACAGGGAAAGGTGACCAAGTGGTTCAATAAC
 TCTGCAGCTTCCCTGACAATGCCAACCCCTGGACAACATCCGTTCAGCCTCATCGTGAGTCA
 GGACGTGGTGAAGCTGCAGTGGCTGCTGTGCTCTCCAGAAGAATTGATGGTCCCTGTTGG
 ACTCTGTGCTTCCCTGAGAGTGCCCATCGGCTGAAGTCAAGCATTGAGCTGGTCAATGAAAG
 GCTGCAGATAAGCTGGATCTACCCAGATCGTGAAGATCCTAACTCAGGACACTCCGAGTT
 TTTTATAGACCAAGGCCATGCCAAGGTGGCCAACTGATCGTGTGGAAGTGTTCCTCCA
 GTGAAGCCCTCCGCCCTTGTACCCCTGGCATCGAAGCCAGCTCGGAAGCTCAGTTTAC
 ACCAAAGGTGACCAACTTATACTCAACTGAAATAACATCAGCTCTGATCGGATCCAGCTGAT
 GAACTCTGGATTGGCTGGTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCC
 ACTCCATCCTGCTGCCGAACCAGAAATGCCAAATTAGATCTGGGTCCCAGTGTCAATTGGT
 AAGGCCTTGGGATTGAGGCAGCTGAGTCCTCACTGACCAAGGATGCCCTGTGCTTACTCC
 AGCCTCCTTGTGGAAACCCAGCTCCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAG
 GGAAGGCTGGTCCCAGCTGGAGTATGGGTGTGAGCTCTAGACCATCCCTCTGCAAT
 CAATAAACACTTGCCTGTGAAAAA

FIGURE 72

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881
><subunit 1 of 1, 484 aa, 1 stop
><MW: 52468, pI: 7.14, NX(S/T): 3
MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELDHNATSILQQPLLSAM
REKPAGGI PVLGSLVNTVLKHIIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPL
VKTIVEFHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMN
LLVPSLPNLVKNQLCVPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDTIQLYL
GAKLLDSQGKVTKWFFNSAASLTMPTLDNIPFSLIVSQDVKAAVAAVLSPEEFMVLLDSVL
PESAHLRKSSIGLINEKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSEAI
RPLFTLGIEASSEAQFYTKGDQLILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEIIHSIL
LPNQNGKLRSRGVPVSLVKALGFEEAAESSLTKDALVLTPASLWKPSSPVSQ
```

Important features of the protein:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 48-51, 264-267, 401-404

Glycosaminoglycan attachment site.

amino acids 412-415

LBP / BPI / CETP family proteins.

amino acids 407-457

FIGURE 73

GAGCGAAC**ATG**GCAGCGCGTGGCGTTGGTGTCTGTGACCATGGTGGTGGCGCTG
 CTCATCGTTGCGACGTTCCCTCAGCTCTGCCAAAGAAAAGAAGGAGATGGTGTATCTGA
 AAAGGTTAGTCAGCTGATGGAATGGACTAACAAAAGACCTGTAATAAGAAATGAATGGAGACA
 AGTTCCGTCGCCTGTGAAAGCCCCACCGAGAAATTACTCCGTTATCGTCATGTTCACTGCT
 CTCCAACGTGATAGACAGTGTGCGTTGCAAGCAAGCTGATGAAGAATTCCAGATCCTGGC
 AAACCTCTGGCGATACTCCAGTGCATTACCAACAGGATATTTTGCCATGGTGGATTTG
 ATGAAGGCTCTGATGTATTCAGATGCTAACATGAATTCACTGAGTTACAGGTGCGGGGTTTCAGC
 TGAGCAGATTGCCCGGTGGATGCCGACAGAACTGATGTCATAATTAGAGTGATTAGACCCC
 CAAATTATGCTGGTCCCCTATGTTGGGATTGCTTTGGCTGTTATTGGTGGACTTGTGTAT
 CTTCGAAGAAGTAATATGAAATTCTCTTTAATAAAACTGGATGGCTTTGCAGCTTGTG
 TTTGTGCTTGCTATGACATCTGGTCAAATGTGGAACCATATAAGAGGACCACCATATGCC
 ATAAGAATCCCCCACACGGGACATGTGAATTATCCATGGAAGCAGTCAGCCCAGTTGTA
 GCTGAAACACACATTGTTCTCTGTTAATGGTGGAGTTACCTTAGGAATGGTGTGGCTGGTATTG
 TGAAGCTGCTACCTCTGACATGGATATTGGAAAGCGAAAGATAATGTGTGGCTGGTATTG
 GACTTGTGTATTATTCTTCAGTTGGATGCTCTATTAGATCTAAATATCATGGCTAC
 CCATACAGCTTCTGATGAGT**TAA**AAAGGTCCCAGAGATATAGACACTGGAGTACTGGAA
 ATTGAAAAACGAAAATCGTGTGTGTTGAAAAGAAGAATGCAACTGTATATTGTATTAC
 CTCTTTTTCAAGTGATTTAAATAGTTAATCATTAAACCAAGAAGATGTGTAGTGCCTTA
 ACAAGCAATCCTCTGTCAAAATCTGAGGTATTGAAAATAATTATCCTCTAACCTCTCTT
 CCCAGTGAACCTTATGGAACATTAAATTAGTACAATTAAAGTATATTATAAAATTGTAAAA
 CTACTACTTGTGTTAGTTAGAACAAAGCTAAAACACTTTAGTTAATTGGTCATCTGAT
 TTTATATTGCCTTATCCAAAGATGGGAAAGTAAGTCCTGACCAGGTGTCACATATGCC
 TGTTACAGATAACTACATTAGGAATTCTAGCTTCTCATCTTGTTGATGTGTAT
 ACTTTACGCATCTTCCTTTGAGTAGAGAAAATTATGTGTGTATGTGGCTTCTGAAAATG
 GAACACCATTCTCAGAGCACACGTCTAGCCCTCAGCAAGACAGTTGTTCTCCTCCT
 GCATATTCTACTGCGCTCAGCCTGAGTGATAGAGTGTGAGACTCTGTCTAAAAAAAAAGTA
 TCTCTAAATACAGGATTATAATTCTGCTTGAGTATGGTGTAACTACCTGTATTAGAAA
 GATTTCAGATTCCATCTCCTTAGTTCTTAAAGGTGACCCATCTGTGATAAAAATA
 TAGCTTAGTGCTAAAATCAGTGTAACTTACATGGCCTAAAATGTTCTACAAATTAGAGT
 TTGTCACTTATTCCATTGTACCTAAGAGAAAATAGGCTCAGTTAGAAAAGGACTCCCTGG
 CCAGGCGCAGTGACTTACGCCTGTAATCTCAGCACTTGGGAGGCCAAGGCAGGCAGATCAC
 GAGGTGAGGAGTCGAGACCATTGGCCAACATGGTGAAACCCGTCTACTAAAATAT
 AAAAATTAGCTGGGTGTGGTGGCAGGAGCCTGTAATCCCAGCTACACAGGAGGCTGAGGCAC
 GAGAATCACTGAACTCAGGAGATGGAGGTTTCAGTGAGCCGAGATCACGCCACTGCACTCC
 AGCCTGGCAACAGAGCGAGACTCCATCTAAAAAAAAAAAAAA

FIGURE 74

MAARWRFWCVSVTMVALLIVCDVPSASAQRKKEMVLSEKVSQMLEWTNKRPVIRMNGDKFR
RLVKAPPRNYSVIVMFTALQLHRQCVVCKQADEEFQILANSWRYSSAFTNRIFFAMVDFDEG
SDVFQMLNMNSAPTFINFPAKGKPKRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNY
AGPLMLGLLLAVIGGLVYLRRSNMEFLFNKTGWAFAALCFVLAMTSGQMWNHIRGPPYAHKN
PHTGHVNYIHGSSQAQFVAETHIVLLFNGGVTLGMVLLCEAATS DMDIGKRKIMCVAGIGLV
VLFFSWMLSIFRSKYHGYPYSFLMS

Signal peptide:

amino acids 1-29

Transmembrane domains:

amino acids 183-205, 217-237, 217-287, 301-321

FIGURE 76

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64885
<subunit 1 of 1, 536 aa, 1 stop
<MW: 61450, pI: 9.17, NX(S/T): 7
MLLWVSVVAALALAVLAPGAGEQRRRAAKAPNVVLVVSDSFDGRLTFHPGSQVVKLPFINF
MKTRGTSFLNAYTNSPICCPSSRAAMWSGLFTHLTESWNNFKGLDPNYTTWMDVMERHGYRTQ
KFGKLDYTSGHHSISNRVEAWTRDVAFLRQEGRPMVNLLIRNRTKVRVMERDWQNTDKAVNW
LRKEAINYTEPFVIYLGLNLPHYPSPSSGENFGSSTFHTSLYWLEKVSHDAIKIPKWSPLS
EMHPVDYYSSYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQLDLLQKTIVIY
SSDHGELAMEHRQFYKMSMYEASAHVPLLMMGPGIKAGLQVSNVSVSLVDIYPTMLDIAGIPL
PQNLSGYSLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYSDGAS
ILPQLFDLSSDPDELTNAVFKPEITYSLDQKLHSIINYPKVSASVHQYNKEQFIWKQSIG
QNYNSVIANLRWHQDWQKEPRKYENAIIDQWLKTHMNPRAV
```

Important features:

Signal peptide:

amino acids 1-15

N-glycosylation sites.

amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,
498-501

Sulfatases proteins:

amino acids 286-315, 359-369, 78-97

FIGURE 77

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAG
 AGCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCACTGAGAGGTCTGCC**ATG**
 GCCTCTTGGCCTCCAACTTGTGGGCTACATCCTAGGCCTCTGGGGCTTTGGCACACT
 GGTTGCCATGCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTCGGTGCCAGCATTGTGACAG
 CAGTTGGCTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAG
 TGTGACATCTATAGCACCCCTCTGGGCTGCCGCTGACATCCAGGCTGCCAGGCCATGAT
 GGTGACATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTTGGCATGAGATGCA
 CAGTCTCTGCCAGGAATCCCGAGCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTC
 ATCCTTGGAGGCCTCTGGGATTCAATTCTGTGCCTGGAATCTCATGGGATCCTACGGGA
 CTTCTACTCACCCTGGTGCCTGACAGCATGAAATTGAGATTGGAGAGGGCTTTACTTGG
 GCATTATTTCTTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTCTGCTCATCC
 CAGAGAAATCGCTCCAACTAACGATGCCTACCAAGCCCCAACCTCTGCCACAAGGAGCTC
 TCCAAGGCCTGGTCAACCTCCAAAGTCAGAGTGAGTTCAATTCTACAGCCTGACAGGGT
 ATGTG**TGA**AGAACCAAGGGCCAGAGCTGGGGGTGGCTGGTCTGTGAAAAAACAGTGGACAG
 CACCCCGAGGGCCACAGGTGAGGGACACTACCAACTGGATCGTGTCAAGAGTGCTGCTGAGG
 ATAGACTGACTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGGCTAGTGTAAACAGCATG
 CAGGTTGAATTGCCAAGGATGCTGCCATGCCAGCCTTCTGTTCTCACCTGCTGCTC
 CCCTGCCCTAACGTCCCCAACCTCAACTTGAAACCCCATTCCCTTAAGCCAGGACTCAGAGG
 ATCCCTTGCCTCTGGTTACCTGGACTCCATCCCCAACCCACTAACATCACATCCACTG
 ACTGACCCCTGTGATCAAAGACCCTCTCTGGCTGAGGTTGGCTTAGCTCATTGCTGG
 GGATGGGAAGGAGAAGCAGTGGCTTGTGGCATTGCTCTAACCTACTTCTCAAGCTTCCC
 TCCAAAGAAACTGATTGGCCCTGGAACCTCCATCCACTTGTATGACTCCACAGTGTCC
 AGACTAATTGTGCATGAACTGAAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAG
 GATGCAGGATGGGAGGACAGGAAGGCAGCCTGGACATTAAAAAAATA

FIGURE 78

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64886
><subunit 1 of 1, 230 aa, 1 stop
><MW: 24549, pI: 8.56, NX(S/T): 1
MASLGLQLVGYILGLLGLLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGIT
QCDIYSTLLGLPADIQAQAMMVTS offense AISSLACIISVVGMRCTVFCQESRAKDRVAVAGGVF
FILGGLLGFIPVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGISSLFSLIAGIILCFSCS
SQRNRSNYYDAYQAQPLATRSSPRPGQPPKVKEFNSYSLTGYV
```

Important features of the protein:

Signal peptide:

amino acids 1-24

Transmembrane domains:

amino acids 82-102, 117-140, 163-182

N-glycosylation site.

amino acids 190-193

PMP-22 / EMP / MP20 family proteins.

amino acids 46-59

FIGURE 79

GCAGTGCTGCTGTCCCCTCAGCTGCTCTGAAGCTCCATGGTGCCAGAATCTCGCTCCTGC
TTATGTGTCAAGTCTGTCTCCTCCTCTTGTGTCCAAGGGAAGTCATCGCTCCGCTGGCTCAG
AACCATGGCTGTGCCAGCCGGCACCCAGGTGTGGAGACAAGATCTACAACCCCTGGAGCAG
TGCTGTTACAATGACGCCATCGTGTCCCTGAGCGAGACCCGCCAATGTGGTCCCCCTGCAC
CTTCTGGCCCTGCTTGAGCTCTGCTGTCTTGATTCCCTTGGCCTCACAAACGATTGTTG
TGAAGCTGAAGGTTCAGGGTGTGAATTCCCAGTGCCACTCATCTCCATCTCCAGTAAATGT
GAAAGCAGAACAGCTTCCTGGAAGACATAGAAAGAAAATCAACTTCACTAAGGCATC
TCAGAACATAGGCTAAGGTAATATGTGTACCAAGTAGAGAAGCCTGAGGAATTACAAATG
ATGCAGCTCCAAGCCATTGTATGGCCATGTGGGAGACTGATGGACATGGAGAATGACAGT
AGATTATCAGGAAATAAAAGTGGTTTCCAATGTACACACCTGTAAAA

FIGURE 80

MVPRIFAPAYVSVC~~LLL~~C~~PREVI~~APAGSEPWL~~CQ~~PAPRCGD~~KI~~YNPLEQCCYND~~AI~~VSLSE
TRQCGPPCTFWPCFELCCLDSFG~~L~~TND~~F~~VVKLKVQGVNSQCHSSPISSKCESRRRF~~P~~

Signal peptide:

amino acids 1-25

FIGURE 81

CTCCACTGCAACCACCCAGAGCC**ATG**GCTCCCCGAGGCTGCATCGTAGCTGTCTTGCATT
TTCTGCATCTCCAGGCTCCTGCTCACACGGAGCCCCAGTGGCCCCATGACTCCTTACCT
GATGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCCTGCAGCACTGTT
GCTATGATGATGCCCGTCGTGCCCTTGGCCAGGACCCAGACGTGGAAACTGCACCTTCAGA
GTCTGCTTGAGCAGTGCTGCCCTGGACCTTCATGGTGAAGCTGATAAACAGAACTGCGA
CTCAGCCGGACCTCGGATGACAGGCTTGTGCGAGTGTCA**TAA**TGGAACATCAGGGAA
CGATGACTCCTGGATTCTCCTCCTGGGTGGGCTGGAGAAAGAGGGCTGGTGTACCTGAGA
TCTGGATGCTGAGTGGCTGTTGGGGCCAGAGAAACACACACTCAACTGCCACTTCATT
CTGTGACCTGTCTGAGGCCACCCCTGCAGCTGCCCTGAGGAGGCCACAGGTCCCCTCTAG
AATTCTGGACAGCATGAGATGCGTGTGCTGATGGGGGCCAGGGACTCTGAACCCCTCTGAT
GACCCCTATGGCCAACATCAACCCGGCACCACCCCAAGGCTGGCTGGGAACCCCTCACCC
TCTGTGAGATTTCCATCATCTCAAGTTCTCTATCCAGGAGCAAAGCACAGGATCATAA
TAAATTATGTACTTTATAAATGAAAA

FIGURE 82

MAPRGCIVAVFAIFCISRLLC SHGAPVAPMTPYLMLCQPHKRCGDKFYDPLQHCCYDDAVVP
LARTQTCGNCTFRVCFEQCCPWTFMVKLINQNCD SARTSDDR LCRSVS

Signal peptide:

amino acids 1-24

FIGURE 83

GGGGGCGGGTGCCTGGAGCACGGCGTGGGCCGCCCCGAGCGCTCACTCGCTCGCACTCAG
 TCGCGGGAGGCTTCCCCGCGCCGGCGTCCCGCCCGCTCCCCGGCACCAAGATTCCTCT
 GCGCGTCCGACGGCGAC**ATGGCGT**CCCCACGCCCTGGAGGCCGGCAGCTGGCGCTGGGA
 TCCCTGCTCTCGCTCTCTTCCGTGGCTCGTCCCTAGGTCCGGTGGCAGCCTCAAGGTCGC
 CACGCCGTATTCCCTGTATGTCTGTCCCAGGGGCAGAACGTACCCTCACCTGCAGGCTCT
 TGGGCCCTGTGGACAAAGGGCACGATGTGACCTCTACAAGACGTGGTACCGCAGCTCGAGG
 GGCAGGGTGAGACCTGCTCAGAGGCCGGCCATCCGCAACCTCACGTTCCAGGACCTTCA
 CCTGCACCATGGAGGCCACCAGGCTGCCAACACCAGCCACGACCTGGCTAGCGCACGGGC
 TGGAGTCGGCCTCCGACCACCATGGCAACTTCTCCATCACCATGCGCAACCTGACCCCTGCTG
 GATAGCGGCCTCTACTGCTGCCTGGTGGAGATCAGGCACCACACTGGAGCACAGGGT
 CCATGGTGCCATGGAGCTGCAGGTGCAGACAGGCAAAGATGCACCATCCAACACTGTGTGGTGT
 ACCCATCCTCCCAGGATAGTGAACACATCACGGCTGCAGCCCTGGTACGGGTGCCTGC
 ATCGTAGGAATCCTCTGCCTCCCCCTCATCCTGCTCCTGGTCTACAAGCAAAGGCAGGCAGC
 CTCCAACCGCCGTGCCAGGAGCTGGTGCAGACAGCAACATTCAAGGGATTGAAAACC
 CCGGCTTGAAGCCTCACCACCTGCCAGGGATAACCGAGGCCAAAGTCAGGCACCCCTG
 TCCTATGTGGCCAGCGGCAGCCTCTGAGTCGGCGCATCTGCTTCGGAGGCCAGCAC
 CCCCCTGTCCTCCAGGCCCCGGAGACGTCTTCCATCCCTGGACCCCTGTCCTGACT
 CTCCAAACTTGAGGTCACT**TAG**CCCAGCTGGGGACAGTGGCTGTTGGCTGGGTCTGG
 GGCAGGGTGCATTGAGCCAGGGCTGGCTCTGTGAGTGGCCTCCTGGCCTGGCCCTGGTTC
 CCTCCCTCCTGCTCTGGCTCAGATACTGTGACATCCCAGAAGCCCAGCCCTCAACCCCTC
 TGGATGCTACATGGGATGCTGGACGGCTCAGCCCTGTTCCAAGGATTGGGGTGTGAG
 ATTCTCCCTAGAGACCTGAAATTACCACTACAGATGCCAAATGACTTACATCTTAAGAA
 GTCTCAGAACGTCCAGCCCTCAGCAGCTCTGTTCTGAGACATGAGCCTGGGATGTGGCA
 GCATCAGTGGACAAGATGGACACTGGGCCACCCCTCCAGGCACCAGACACAGGGCACGGT
 GAGAGACTCTCCCCGTGGCGCCTGGCTCCCCGTTTGGCCAGGGCTGCTCTGT
 AGACTTCCCTTTGTACCACTGGCTCTGGGCCAGGCCTGCCACTGGCCATGCC
 ACCTTCCCCAGCTGCCCTACCAGCAGTTCTGAAGATCTGTCAACAGGTTAAGTCAAT
 CTGGGGCTCCACTGCCTGCATTCCAGCTCCAGAGCTGGTGGTCCGAAACGGGAAGTAC
 ATATTGGGGCATGGTGGCTCCGTGAGCAAATGGTGTCTGGCAATCTGAGGCCAGGACAG
 ATGTTGCCCAACCACTGGAGATGGCTGAGGGAGGTGGTGGGCTTCTGGGAAGGTGA
 GTGGAGAGGGGCACCTGCCCTCCGCCCCATCCCCTACTCCACTGCTCAGCGCGGGCC
 ATTGCAAGGGTGCACACAATGTCTGTCCACCCCTGGGACACTTCTGAGTATGAAGCAGGGAT
 GCTATTAAAAACTACATGGGAAAAAAAAAAAAAAAAAAAAAAAAGA

FIGURE 84

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64897
><subunit 1 of 1, 311 aa, 1 stop
><MW: 33908, pI: 6.87, NX(S/T): 6
MGVPTALEAGSWRWGSLLFALFLAASLGPVAAFKVATPYSLYVCPEGQNVTLTCRLLGPVDK
GHDVTFYKTWYRSSRGEVQTCERRPIRNLTFQDLHLHHGGHQAANTSHDLAQRHGLEASD
HHGNFSITMRNLTLDSGLYCCLVVEIRHHSEHRVHGAMELQVQTGKDAPSNCVVYPSSQ
DSENITAAALATGACIVGILCLPLLLLVYKQRQAASNRRAQELVRMDSNIQGIENPGFEAS
PPAQGipeAKVRHPLSYVAQRQPSESGRHLLSEPSTPLSPPGPGDVFVFPSDLPPDSPNFEVI
```

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 190-216

FIGURE 85

CCCACGCGTCCGCCTCTCCCTCTGGACCTTCCTCGTCTCCATCTCTCCCTCCT
 TTCCCCGCGTTCTCTTCCACCTTCTCTTCTCCCACCTAGACCTCCCTGCCCTCC
 TTTCTGCCACCCTGCTTCCTGGCCCTCTCCGACCCGCTCTAGCAGCAGACCTCCTGG
 GGTCTGTGGGTTGATCTGTGGCCCTGTGCCTCCGTGTCCTTCGTCTCCCTCCCGA
 CTCCGCTCCGGACCAGCGGCCTGACCTGGGAAAGG**ATG**GTTCCGAGGTGAGGGTCCTC
 TCCTCCTTGCTGGACTCGCGCTGCTCTGGTCCCCCTGGACTCCCACGCTCGAGCCGCC
 AGACATGTTCTGCCTTTCCATGGGAAGAGATACTCCCCCGCGAGAGCTGGCACCCCTACT
 TGGAGCCACAAGGCCTGATGTACTGCCTGCCTGTACCTGCTCAGAGGGCCCATGTGAGT
 TGTACCGCCTCCACTGTCCGCCTGTCCACTGCCCGCAGCCTGTGACGGAGGCCACAGCAATG
 CTGTCCTAACGTGTGGAACCTCACACTCCCTCTGGACTCCGGGCCCCACCAAAGTCCTGCC
 AGCACAAACGGGACCATGTACCAACACGGAGAGATCTCAGTGCCTGAGCTGTTCCCTCC
 CGCCTGCCAACCAACAGTGTGTCCCTGCAGCTGCACAGAGGGCCAGATCTACTGCCCTCAC
 AACCTGCCCGAACCAAGGCTGCCAGCACCCCTCCACTGCCAGACTCCTGCTGCCAACGCT
 GCAAAGATGAGGCAAGTGAAGCAATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGTG
 AGACATCCTCAGGATCCATGTTCCAGTGATGCTGGAGAAAGAGAGGGCCGGCACCCAGC
 CCCCACGGCCTCAGGCCCTCTGAGCTTCATCCCTGCCACTTCAGACCCAAGGGAGCAG
 GCAGCACAACTGTCAAGATCGCCTGAAGGAGAAACATAAGAAAGCCTGTGCAATGGCGGG
 AAGACGTACTCCCACGGGAGGTGTGGCACCCGGCTTCCGTGCCTCGGCCCTTGCCCTG
 CATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCCACCGAGT
 ACCCCTGCCGTACCCCGAGAAAGTGGCTGGAAAGTGCTGCAAGATTGCCAGAGGGACAAA
 GCAGACCCCTGGCCACAGTGAGATCAGTTCTACCAGGTGTCCTGGCACGGCCGGGTCT
 CGTCCACACATCGGTATCCCCAAGCCCAGACAAACCTGCCTCGCTTGCCCTGGAACACGAGG
 CCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAGATGAGGAAACTGAGGCTCAG
 AGAGGTGAAGTACCTGGCCAAGGCCACACAGCCAGAACTTCCACTTGACTCAGATCAAGA
 AAGTCAGGAAGCAAGACTTCCAGAAAGAGGCACAGCACCCGACTGCTCGCTGGCCCCAC
 GAAGGTCACTGGAACGTCTCCTAGCCCAGACCTGGAGCTGAAGGTACGGCCAGTCCAGA
 CAAAGTGACCAAGACATAACAAAGACC**TAA**CAGTTGCAGATATGAGCTGTATAATTGTT
 ATTATATATTAATAATAAGAAGTTGCATTACCCCTAAAAAAAAAAAAAAA

FIGURE 86

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902
><subunit 1 of 1, 451 aa, 1 stop
><MW: 49675, pi: 7.15, NX(S/T): 1
MVPEVRVLSSLLGLALLWFPLDSHARARPDMFCLFHGKRYSPGESWHPYLEPQGLMYCLRCT
CSEGAHVSCYRLHCPPVHCPQPVTEPQQCCPKCVEPHTPSGLRAPPKSCQHNGTMYQHGEIF
SAHELFPSRLPNQCVCVLCSCTEGQIYCGLTTCPGPAPLPLPDSCCQACKDEASEQSDEED
SVQSLHGVRHPQDPCSSDAGRKRGPGTAPGTGLSAPLSFIPRHFTRPKGAGSTTVKIVLKEKH
KKACVHGGKTYSHGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPTEYPCRHPEKVAGKC
CKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRRALEHEASDLVEIYLWKLV
KDEETEAQRGEVPGPRPHSQNLPLSDQESQEARNPERGTALPTARWPPRRSLERLPSPDPG
AEGHGQSRQSDQDITKT
```

Signal peptide:

amino acids 1-25

FIGURE 87

CTAGCCTGCGCCAAGGGTAGTGAGACCGCGCGAACAGCTTGC GGCTGC GGGGAGCTCCC
GTGGCGCTCCGCTGGCTGTGCAGGCGGCCATGGATTCTTGCGAAAATGCTGATCTCAGT
CGCAATGCTGGCGCAGGGCTGGCGTGGCTACCGCCTCGTTATCGTACCCCCGGAG
AGCGCGGAAGCAGGAAATGCTAAAGGAGATGCCACTGCAGGACCCAAAGGAGCAGGGAGGAG
GCGCCAGGACCCAGCAGCTATTGCTGCCACTCTGCAGGAGGCAGCGACCACGCAGGAGAA
CGTGGCCTGGAGGAAGAACTGGATGGTGGCGCGAAGGC GGCGCAGCGGGAGGTACCGT
GAGACCGGACTTGCCTCCGTGGCGCCGGACCTGGCTGGCGCAGGAATCCGAGGCAGCC
TTTCTCCTCGTGGGCCAGCGGAGAGTCCGGACCGAGATAACCATGCCAGGACTCTCCGGGG
TCCTGTGAGCTGCCGTGGTGAGCACGTTCCCCAACCCCTGGACTGACTGCTTAAGGT
CCGCAAGGC GGCCAGGGCCAGACGCGAGTCGGATGTGGTGAAGTGAACCAACCAATAAAA
TCATGTT CCTCCAAAAA AAAAAAAAAAAAAA AAAAAAAAAAAAAA AAAAAAAAAAAAAA
AAAAAAAAAAA

FIGURE 88

MDSLRKMLISVAMLGAGAGVGYALLVIITPGERRKQEMILKEMPLQDPRSREEAARTQQLLLA
TLQEAAATTQENVVAWRKNWMVGEGGASGRSP

Signal peptide:

amino acids 1-18

FIGURE 89

CAGGAGAGAAGGCACCGCCCCACCCGCCTCAAAGCTAACCTCGGGCTTGAGGGGAAGA
 GGCTGACTGTACGTTCTTACTCTGGCACCCTCTCCAGGCTGCC**ATG**GGGCCAGCAC
 CCTCTCCTCATCTTGTTCCTTGTATGGTCGGGACCCCTCCAAGGACAGCAGCACCACCT
 TGTGGAGTACATGGAACGCCGACTAGCTGCTTAGAGGAACGGCTGGCCAGTGCCAGGACC
 AGAGTAGTCGGCATGCTGAGCTGCGGGACTTCAAGAACAAAGATGCTGCCACTGCTGGAG
 GTGGCAGAGAAGGAGCAGGGAGGCAGTCAGAACTGAGGCCGACACCCTCCGGGAGAGTGG
 TCGTCTGGAGCAGGGAGGTAGACTATCTGGAGACCCAGAACCCAGCTCTGCCCTGTAGAGT
 TTGATGAGAAGGTGACTGGAGGCCCTGGACCAAAGGCAAGGAAGAAGGAATGAGAAGTAC
 GATATGGTACAGACTGTGGCTACACAATCTCAAGTGAGATCAATGAAGATTCTGAAGCG
 ATTGGTGGCCAGCTGGTCTATGGACCAAGGATCCACTGGGCAAACAGAGAAGATCTACG
 TGTAGATGGACACAGAACATGACACAGCCTTGTCTTCCAAGGCTGCGTACTTCACCCT
 GCCATGGCTGCCCGGAAAGCTCCCAGTCCGGTGCCTCCCTGGTAGGCACAGGGCA
 GCTGGTATATGGTGGCTTCTTATTGCTCGAGGCCTCCTGGAAGACCTGGTGGAGGTG
 GTGAGATGGAGAACACTTGCAGCTAACATTCCACCTGGCAAACCGAACAGTGGTGGAC
 AGCTCAGTATTCCCAGCAGAGGGCTGATCCCCCTACGGCTTGACAGCAGACACCTACAT
 CGACCTGGTAGCTGATGAGGAAGGTCTTGGCTGTCTATGCCACCCGGGAGGATGACAGGC
 ACTTGTGTCGCCAAGTTAGATCCACAGACACTGGACACAGAGCAGCAGTGGACACACCA
 TGTCCCAGAGAGAACATGCTGAGGCTGCCCTGTATCTGGGACCCCTATGTCGTCTATAA
 CACCCGTCCTGCCAGTCGGCCGCATCCAGTGCTCCTTGATGCCAGCGGCACCCGTACCC
 CTGAACGGCAGCAGCTCCCTATTTCGGCAGATATGGTGCCTGCCAGCCTCCGCTAT
 AACCCCGAGAACGCCAGCTATGCCCTGGGATGATGGCTACCAAGATTGTCTATAAGCTGGA
 GATGAGGAAGAAAGAGGAGGGAGGTT**TGA**GGAGCTAGCCTGTTTGCACTTTCTCACTC
 CCATACATTATATTATATCCCCACTAAATTCTTGTTCCTCATTCTCAAATGTGGCCAG
 TTGTGGCTCAAATCCTCTATATTTAGCCAATGGCAATCAAATTCTTCAGCTCCTTGTT
 TCATACGGAACTCCAGATCCTGAGTAATCCTTAGAGGCCGAAGAGTCAAACCCCTCAATG
 TTCCCTCCTGCTCCTGCCCATGTCAACAAATTCAAGGCTAACGGATGCCAGGCCAGG
 GCTCTAACCTGTATGCCAGGGCAGGCCAGGGAGCAGGCAGCAGTGTCTCCCTCACTCCCT
 ACTTGGGGAGGGAGAAATAGGAGGAGACGTCCAGCTGTCTCTTCCACTCCTCC
 TCAGTGTCTGAGGAACAGGACTTCTCCACATTGTTGTATTGCAACATTGCAATTAAA
 AGGAAAATCCACAAAAAA
 AAAAAAAAAAAAAAA

FIGURE 90

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64905
<subunit 1 of 1, 406 aa, 1 stop
<MW: 46038, pI: 6.50, NX(S/T): 2
MGPSTPLLILFLLSGPLQGQQHHLVEYMERLAALERLAQCQDQSSRHAELRDFKNKM
LPLLEVAEKEREALRTEADTISGRVDRLEREVDYLETQNPALPCVEFDEKVTGGPGTKGKGR
RNEYDMVTDCGYTISQVRSMKILKRFGGPAGLWTKDPLGQTEKIYVLDGTQNDTAFVFPR
RDFTLAMAARKASRVRVFPWVGTGQLVYGGFLYFARRPPGRPGGGEMENTLQLIKFHLAN
RTVVDSVFPAGEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCLAKLDPQTLDTEQ
QWDTPCPRENAAAFVICGTLIVVVYNTRPASRARIQCSFDASGTLTPERAALPYFPRRYGAH
ASLRYNPRERQLYAWDDGYQIVYKLEMRKKEEEV
```

Important features:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 177-180, 248-251

FIGURE 91

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTGCCCTCGCTCACGCAG
 AGCCTCTCCGTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTCTCTCTAATCCAT
 CCGTCACCTCTCCTGTCATCCGTTCCATGCCGTGAGGTCCATTACAGAACACATCC**ATGG**
 CTCTCATGCTCAGTTGGTTCTGAGTCTCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTT
 GGGCCAGACAAGCCTGTCCAGGCCTGGTGGGGGAGGACGCAGCATTCTCCTGTTCTGTC
 TCCTAAGACCAATGCAGAGGCCATGGAAGTGCGGTTCTCAGGGCCAGTTCTCTAGCGTGG
 TCCACCTCTACAGGGACGGGAAGGACCAGCATTATGCAGATGCCACAGTATCAAGGCAGG
 ACAAAACTGGTGAAGGATTCTATTGCGGAGGGCGCATCTCTGAGGCTGGAAAACATTAC
 TGTGTTGGATGCTGGCCTATGGGTGCAGGATTAGTCCCAGTCTTACTACCAGAAGGCCA
 TCTGGGAGCTACAGGTGTCAGCACTGGCTCAGTCCTCTCATTCCATCACGGGATATGTT
 GATAGAGACATCCAGCTACTCTGTCAGTCCTCTGGTCCCCCGGCCACAGCGAAGTG
 GAAAGGTCCACAAGGACAGGATTGTCCACAGACTCCAGGACAAACAGAGACATGCATGGCC
 TGTTGATGTGGAGATCTCTGACCGTCCAAGAGAACGCCGGAGCATATCCTGTTCCATG
 CGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAAGGAGATACTTTTGA
 GCCTATATCGTGGCACCTGGTACCAAAGTACTGGGAATACTCTGCTGTGGCCTATTTTTG
 GCATTGTTGGACTGAAGATTCTTCTCAAATTCCAGTGGAAAATCCAGGCGGAACGGAC
 TGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCGGAAACACGCAGTGGAGGTGAC
 TCTGGATCCAGAGACGGCTACCCGAAGCTCTGCGTTCTGATCTGAAAAGTGTAAACCCATA
 GAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTACAAGGAAGAGTGTGGCT
 TCTCAGAGTTCCAAGCAGGGAAACATTACTGGGAGGTGGACGGAGGACACAATAAGGTG
 GCGCGTGGGAGTGTGCCGGATGATGTGGACAGGAGGAAGGAGTACGTGACTTGTCTCCG
 ATCATGGGTACTGGGTCTCAGACTGAATGGAGAACATTGTATTCACATTAAATCCCCGT
 TTTATCAGCGTCTCCCCAGGACCCCACCTACAAAATAGGGTCTTCTGGACTATGAGTG
 TGGGACCATCTCCTCTTCAACATAATGACCAGTCCCTTATTATACCCGTGACATGTCGGT
 TTGAAGGCTATTGAGGCCCTACATTGAGTATCCGTCTATAATGAGCAAAATGGAACCTCC
 ATAGTCATCTGCCAGTCACCCAGGAATCAGAGAAAGAGGCCTTGGCAAAGGGCCTCTGC
 AATCCCAGAGACAAGCAACAGTGAGTCCTCCTCACAGGCAACCACGCCCTCCTCCCCAGGG
 GTGAAATG**TAG**GATGAATCACATCCCACATTCTTCTTAGGGATATTAAGGTCTCTCCCA
 GATCCAAAGTCCCGAGCAGCCGGCAAGGTGGCTTCCAGATGAAGGGGACTGGCCTGTCC
 ACATGGGAGTCAGGTGTCATGGCTGCCCTGAGCTGGGAGGGAAGAAGGCTGACATTACATT
 AGTTGCTCTCACTCCATCTGGCTAAGTGATCTGAAATACCACCTCTCAGGTGAAGAACCG
 TCAGGAATTCCCATCTCACAGGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGC
 TTAGATCTTATTGATGACAGAGTGTATCCTAATGGTTGTCATTATATTACACTTCAGTA
 AAAAAA

FIGURE 92

MALMLSLVLSLLKLGSQWQVFGPDKPQALVGEDAASFCLSPKTNAEAMEVRFFRGQFSS
VVHLYRDGKDQPFMOMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISQSYYQK
AIWELQVSALGSVPPLISITGYVDRDIQLLCQSSGFPRPTAKWKGPQGQDLSTDRTNRDMH
GLFDVEISLTVOENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLF
FGIVGLKIFFSKFQWKIQAELDWRRKHGQAEELRDARKHAVEVTLDPETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFRKSVVASQSFQAGKHYWEVDGGHNKRWRVGVCRDDVDRRKEYVTLS
PDHGYWVLRLNGEHLYFTLNPRFISVFPPRKIGVFLDYECGTISFFNINDQSLIYTLTC
RFEGLLRPYIEYPSYNEQNGTPIVICPVTQESEKEASWQRASAIPETSNSESSSQATTPFLP
RGEM

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 239-255

FIGURE 93

GCGATGGTGCGCCGGTGGCGGTGGCGGCGGTTGCGGAGGCTTCCTGGTCGGATTGCA
 ACGAGGAGAAGATGACTGACCAACCGACTGGCTGAATGAATGAATGGCGAGCCGAGCGC
CATGAGGAGCCTGCCGAGCCTGGCGGCCTGCCCTGTTGTGCTGCGCCGCCGCCGCC
 CCGTCGCCTCAGCCGCCTCGCGGGGAATGTCACCGGTGGCGGGGCCGCCGCCGCC
 GACGCGTCGCCGGGCCCCGGGTGCGGGCGAGCCCAGCCACCCCTCCCTAGGGCGACGGC
 TCCCACGGCCCAGGGCCCCGAGGACCGGGCCCCCGCGGCCACCGTCCACCGACCCCTGGCTG
 CGACTTCTCCAGGCCAGTCCCCGGAGACCACCCCTCTTGGCGACTGCTGGACCCCTTCC
 ACCACCTTCAGGCGCCGCTGGCCCTCGCCGACCACCCCTCCGGCGGCGAACGCACCTC
 GACCACCTCTCAGGGGCCGACCAGACCCGCGCCGACCACCCCTTCGACGACCACGGCCCG
 CGCCGACCACCCCTGAGCGACCACCGTACCGCGCCACGACTCCCCGGACCCGACCCCC
 GATCTCCCCAGCAGCAGCAACAGCAGCGTCTCCCCACCCACCTGCCACCGAGGCCCCCTC
 TTCGCCTCTCCAGAGTATGTAACTGCTCTGTGGTTGGAAGCCTGAATGTGAATCGCT
 GCAACCAGACACAGGGCAGTGTGAGTGTGGCCAGGTATCAGGGCTTCACTGTGAAACC
 TGCAAAGAGGGTTTACCTAAATTACACTTCTGGCTCTGTAGCCATGTGACTGTAGTCC
 ACATGGAGCTCTCAGCATACCGTGAACAGG**TAA**GCAACAGAGGGTGGAACTGAAGTTATT
 TTATTTAGCAAGGGAAAAAAAAGGTGCTACTCTCAAGGACCATACTGGTTAAACAAAG
 GAGGATGAGGGTCAAGATTACAAATATTATATACTTTATTCTACTTTATATGT
 TATATTAATGTCAGGATTAAAAACATCTAATTTACTGATTTAGTTCTC~~AA~~AGCACTAG
 AGTCGCAATTTCTCTGGATAATTCTGAAATTTCATGGAAAAAAATTATTGAAGAAT
 AAATCTGCTTCTGGAGGGCTTCAGGCATGAAACCTGCTAGGGAGTTAGAAATGTTCTT
 ATGTTATTAAATATACCATTGGAGTTGAGGAAATTGTTGTTGGTTATTCTCTCTA
 ATCAAAATTCTACATTGTTCTTGACATCTAAAGCTAACCTGGGGTACCTAATTAA
 TTTAACTAGTGGTAAGTAGACTGGTTACTCTATTACAGTACATTGAGACCAAAAG
 TAGATTAAGCAGGAATTATCTTAAACTATTATGTTATTGGAGGTAAATTAAATCTAGTGG
 ATAATGTACTGTTATCTAACGATTTGCCCTGTACTGCACTGAAAGTAATTATTCTTGACCT
 TATGTGAGGCACCTGGCTTTGTGGACCCCAAGTCAAAAAAACTGAAGAGACAGTATTAAAT
 AATGAAAAAAATAATGACAGGTTATACTCAGTGTAACTGGTATAACCCAAAGATCTGCTGC
 CACTTACGAGCTGTGTTCTGGCAAGTAATTCTTCACTGAGCTTGTCTCTCAAG
 GTTGTGTAAGATTAAATGAGTTGATATATAAAATGCCTAGCACATGTCACTCAATAAA
 TTCTGGTTGTTAAATTCAAAGGAATTATGGACTGAAATGAGAGAACATGTTAAGA
 ACTTTAGCTCTGACAAAGAAGTGTAACTTAGCACTAAATATTAAATGCTTTA
 TAAATGATATTATACTGTTATGGAATTATGTATCATATTGTTATTAAAAATGAGAAG
 AGGCTGGCGCGGTGGCTACGCCTGTAATCCTAGCAGCTTGGGAGGCCAGGCAGGTGGAT
 CACTTGAGGCCAGGAGTTCTAGATGAGCCTGGCCAGCACAGTGAACACCCCGTCTACTAAA
 AATACAAACAAATTAGCTGGCGTGGCAGCACACCTGTAGTCCAGCTACTGGGAGGCT
 GAGGCAGGAGAATCGGTTGAACCCGGGAGGTGGAGGTTGCACTGAGCTGAGATCGCGCCACT
 GCACCTCCAGCCTGGTGAAGAGAGGGAGACTGTCTTAAAAA

FIGURE 94

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952
><subunit 1 of 1, 258 aa, 1 stop
><MW: 25716, pI: 8.13, NX(S/T): 5
MRSLPSLGGLALLCCAAAAAVASAASAGNVTGGGAAGQVDASPGPGLRGEPSHPFPRATA
PTAQAPRTGPPRATVHRPLAATSPAQSPETTPLWATAGPSSTTFQAPLGPSPTPPAAERTS
TTSQAPTRPAPTLSTTGAPTPVATTVPAPTPRTPTDLPSSNSSVLPTPPATEAPS
SPPPEYVCNCVVGSLNVNRCNQTTGQCECRPGYQGLHCETCKEGFYLNYSGLCQPCDCSP
HGALSIPCNR
```

Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation sites.

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

EGF-like domain cysteine pattern signature.

amino acids 214-226.

FIGURE 95

TGC GGCG CAGT GTAG ACCT GGGAGG **ATG** GGC GGC CTG CTG CTGG CTG CTT TCT GGCT TTGG
TCT CGGT GCCC AGGG CCC AGGCC GTG GGT GGG AAG ACT GGAC CCT GAG CAG CTT CTT GGG
CCCT GGTAC GTG CTG CGGT GGC CTCC GGG AAA AGGG CTT GGC ATGG AGA AGG ACAT GAA
GAAC GT CGT GGGGGT GGGT GAC CAG AGT GT CATGG ACCT GATA AAAG CGAA ACT CCGG ATGG
AGCACGGCTGGGAGGGTGTGACCAGAGTGTGACCTGATAAAAGCGAAACTCCGGATGG
GTGTTGAGAATCCCTCAATAGCGTGCTGGAGCTCTGGGTGCTGCCACCAACTCAGAGA
CTATGCCATCATCTCACTCAGCTGGAGTTGGGGACGAGCCCTAACACCGTGGAGCTGT
ACAGTCTGACGGAGACAGCCAGCCAGGAGGCCATGGGCTCTCACCAAGTGGAGCAGGAGC
CTGGGCTTCCTGTCACAG **TAC** CAGGCCAGCTGCAGAAGGACCTCACCTGTGCTACAAGAT
CCTTCTGTGAGTGCTGCGTCCCCAGTAGGGATGGCGCCACAGGGCCTGTGACCTCGGCCA
GTGTCCACCCACCTCGCTAGCGGCTCCGGGCCAGCACCAAGCTCAGAATAAAGCGATT
CACAGCA

FIGURE 96

MGGLLLAFLALVSVPRAQAVWLGRLDPEQLLGPWYVLAVASREKGFAMEKDMKNVVGVVVT
LTPENNLRTLSSQHGLGGCDQSVMIDLICKRNSGWVFENPSIGVLELWVLATNFRDYAIIFTQL
EFGDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

Signal peptide:

amino acids 1-20

FIGURE 97

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCCAGAC**ATG**CTGCTGCTGCTGCTGCC
 CCTGCTCTGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAAACTGCTGACGATGCAGAGTT
 CCGTACGGTGCAGGAAGGCCTGTGTCCATGTGCCCTGCTCCTCTCCTACCCCTCGCAT
 GGCTGGATTTACCTGGCCCAGTAGTCATGGCTACTGGTCCGGGAAGGGGCAATACAGA
 CCAGGATGCTCCAGTGGCCACAAACAACCCAGCTGGCAGTGTGGAGGAGACTCGGGACC
 GATTCCACCTCCTGGGGACCCACATACCAAGAATTGCACCCCTGAGCATCAGAGATGCCAGA
 AGAAGTGATGCGGGGAGATACTTCTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAA
 ACATCACCGGCTCTGTGAATGTGACAGCCTGACCCACAGGCCAACATCCTCATCCCAG
 GCACCCCTGGAGTCCGGCTGCCCTCAGAATCTGACCTGCTCTGTGCCCTGGCCTGTGAGCAG
 GGGACACCCCCATGATCTCCTGGATAGGGACCTCCGTGCCCCCTGGACCCCTCCACAC
 CCGCTCCTCGGTGCTCACCTCATCCCACAGCCCCCAGGACCATGGCACCGCCTCACCTGTC
 AGGTGACCTTCCCTGGGCCAGCGTGACCACGAACAAGACCGTCCATCTAACGTGTCCTAC
 CCGCCTCAGAACTTGACCATGACTGTCTCCAAGGAGACGGCACAGTATCCACAGTCTTGGG
 AAATGGCTCATCTGTCACTCCCAGAGGGCCAGTCTGCGCCTGGTCTGTGCAGTTGATG
 CAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGAGAGGCCTGACCTGTGCCCC
 TCACAGCCCTCAAACCCGGGGTGCTGGAGCTGCCTGGTGCACCTGAGGGATGCAGCTGA
 ATTACACCTGCAGAGCTCAGAACCCCTCGGCTCTCAGCAGGTCTACCTGAACGTCTCCCTGC
 AGAGCAAAGCCACATCAGGAGTGACTIONGGGGTGGTCGGGGAGCTGGAGCCACAGCCCTG
 GTCTTCCCTGCTTCTCGTCATCTCGTTGTAGTGAGGTCTGCAGGAAGAAATCGGCAAG
 GCCAGCAGCGGGCGTGGAGATAAGGGCATAGAGGATGCAAACGCTGTCAGGGTTCAGCCT
 CTCAGGGGCCCTGACTGAACCTGGGCAGAAGACAGTCCCCAGACCAGCCTCCCCAGCT
 TCTGCCCGCTCCTCAGTGGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGT
 GAAGCCTTGGGACTCGCGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCC
 ACAGA**TGA**GAAACTGCAGAGACTCACCTGATTGAGGGATCACAGCCCTCCAGGCAAGGGA
 GAAGTCAGAGGCTGATTCTTGAGAATTAAACAGCCCTAACGTGATGAGCTATGATAACACT
 ATGAATTATGTGCAGAGTGAAAAGCACACAGGCTTAGAGTCAAAGTATCTAAACCTGAAT
 CCACACTGTGCCCTCCCTTTATTTTTAACTAAAAGACAGACAAATTCTA

FIGURE 98

MLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHPCFSYPSHGWIYPGPVVHGYWF
REGANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTLISRARRSDAGRYFFRMEKG
SIKWNYKHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCSPWACEQGTPPMISWIGTSVS
PLDPSTTRSSVLTLIPQPQDHGTSLTCQVTFPGASVTTNKTVHLNVSYPPQNLMTVFQGDG
TVSTVLNGSSLSLPEGQSLRLVCAVDADSNPPARLSLSWRGLTLCPSQPSNPGVLELPWV
HLRDAAEFTCRAQNPLGSQQVYLNVSILQSKATSGVTQGVVGGAGATALVFLSFCVI FVVVR
CRKKSARPAAGVGDTGIEDANAVRG SASQGPLTEPWAEDSPPDQPPPASARSSVGEGELOQYA
SLSFQMVKPWDSRGQEATDTEYSEIKIHR

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 351-370

FIGURE 99

FIGURE 100

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65404
<subunit 1 of 1, 170 aa, 1 stop
<MW: 19457, pI: 9.10, NX(S/T): 0
MKTLFLGVTLGLAAALSFTLEEEDITGTWYVKAMVVDKDFPEDRRPRKVSPVKVTALGGGKL
EATFTFMREDRCIQKKILMRKTEEPGKYSAYGGRKLMYLQELPRRDHYIFYCKDQHHGGLLH
MGKLVGRNSDTNREALEEFKKLVQRKGLSEEDIFTPLQTGSCVPEH
```

Important features:

Signal peptide:

amino acids 1-17

FIGURE 101

GTTCCGCAGATGCAGAGGTTGAGGTGGCTGCAGGACTGGAAGTCATCGGGCAGAGGTCTCAC
AGCAGCCAAGGAACCTGGGGCCCGCTCCTCCCCCTCCAGGCC**ATG**AGGATTCTGCAGTTAA
TCCTGCTTGCCTGGCAACAGGGCTTGTAGGGGGAGAGACCAGGATCATCAAGGGGTTGAG
TGCAAGCCTCACTCCCAGCCCTGGCAGGCAGCCCTGTTGAGAAGACGCGGCTACTCTGTGG
GGCGACGCTCATGCCCGAGATGGCTCCTGACAGCAGCCCAGTGCCTCAAGCCCCGCTACA
TAGTTCACCTGGGGCAGCACAACCTCCAGAAGGAGGGCTGTGAGCAGACCCGGACAGCC
ACTGAGTCCTCCCCACCCGGCTTCAACAAACAGCCTCCCCAACAAAGACCACCGCAATGA
CATCATGCTGGTGAAGATGGCATGCCAGTCTCCATCACCTGGCTGTGCGACCCCTCACCC
TCTCCTCACGCTGTGTCAGTGGCACCAGCTGCCTCATTTCCGGCTGGGGCAGCACGTCC
AGCCCCCAGTTACGCCGCCTCACACCTTGCATGCCAACATCACCATCATTGAGCACCA
GAAGTGTGAGAACGCCAACCCGGAACATCACAGACACCATGGTGTGCCCCAGCGTGCAGG
AAGGGGGCAAGGACTCCTGCCAGGGTGAUTCCGGGGCCCTCTGGTCTGTAACCAGTCTCTT
CAAGGCATTATCTCCTGGGCCAGGATCCGTGCGATCACCCGAAAGCCTGGTGTCTACAC
GAAAGTCTGCAAATATGTGGACTGGATCCAGGAGACGATGAAGAACAA**TAG**ACTGGACCCA
CCCACCACAGCCCATCACCCCTCATTCCACTTGGTGTGTTGGTCTGTTCACTCTGTTAAT
AAGAAACCTAAGCCAAGACCCCTACGAACATTCTTGGCCTCCTGGACTACAGGAGATG
CTGTCACTTAATAATCAACCTGGGTTGAAATCAGTGAGACCTGGATTCAAATTCTGCCTT
GAAATATTGTGACTCTGGGAATGACAACACCTGGTTGTTCTGTTGATCCCCAGCCCCA
AAGACAGCTCCTGGCCATATATCAAGGTTCAATAAATATTGCTAAATGAAAAAAA
AAAAAAAAAAAAAAAAAAAAAA

FIGURE 102

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65405
<subunit 1 of 1, 250 aa, 1 stop
<MW: 27466, pI: 8.87, NX(S/T): 4
MRILQLILLALATGLVGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLAAH
CLKPRYIVHLGQHNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSITW
AVRPLTLSSRCVTAGTSCLISGWGSTSSPQLRLPHTLRCANITIIEHQKCENAYPGNITDTM
VCASVQEQQGDSCQGDGGPLVCNQSLQGIISWGQDPCAIRKPGVYTKVCKYVDWIQETMKNN
```

Important features:

Signal peptide:

amino acids 1-18

Serine proteases, trypsin family, histidine active site.

amino acids 58-63

N-glycosylation sites.

amino acids 99-102, 165-168, 181-184, 210-213

Glycosaminoglycan attachment site.

amino acids 145-148

Kringle domain proteins.

amino acids 197-209, 47-64

Serine proteases, trypsin family, histidine protein

amino acids 199-209, 47-63, 220-243

Apple domain proteins

amino acids 222-249, 189-222

FIGURE 103

GAGCAGTGTCTGCTGGAGCCG**ATG**CCAAAACCATGCATTCTTATTCA
GAGATTGCTCAGAGACAAAAGAAAGAGGAGAGCACCGAAGAA
GTGAAAATAGAAGTTGCATCGTCCAGAAA**ACTG**CTAAGACAAGCAAGAAGGGAGACCT
ACTAAATGCCATTATGACGGCTACCTGGCTAAAGACGGCTCGAAATTCTACTGCAGCCGGA
CACAAAATGAAGGCCACCCAAATGGTTGTTGGTGGCAAGTCATAAAAGGCCTA
GACATTGCTATGACAGATATGTGCCCTGGAGAAAAGCGAAAAGTAGTTACCCCCCTTCATT
TGCATACGGAAAGGAAGGCTATGCAGAAGGCAAGATTCCACCGGATGCTACATTGATTTTG
AGATTGAACATTATGCTGTGACCAAAGGACCACGGAGCATTGAGACATTAAACAAATAGAC
ATGGACAATGACAGGCAGCTCTAAAGCCGAGATAAACCTCTACTTGCAAAGGAATTGAA
AAAAGATGAGAAGCCACGTGACAAGTCATATCAGGATGCAGTTAGAAGATATTTAAGA
AGAATGACCATTGATGGTGATGGCTTCATTCTCCCAAGGAATACAATGTATA
AAACAAAGTCACTTTCTCCAAGTTGTATTCGCTATTTCCCCTATGAGAAGATATTTGAA
TCTCCCCAATACATTGATTTGGTATAATAATGTGAGGCTGTTGCAAACCTAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 104

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65406
<subunit 1 of 1, 222 aa, 1 stop
<MW: 25794, pI: 6.24, NX(S/T): 1
MPKTMHFLFRFIVFFYLWGLFTAQRQKKEESTEEVKIEVLHRPENCSKTSKKGDLLNAHYDG
YLAKDGSKFYCSRTQNEGHPKWFVLGVGQVIKGLDIAMTDMCPGEKRKVVIIPPSFAYGKEGY
AEGKIPPDATLIFEIELYAVTKGPRSIEFKQIDMDNDRQLSKAEINLYLQREFEKDEKPRD
KSYQDAVLEDIFKKNDHDGDGFISPKEYNVYQHDEL
```

Important features:

Endoplasmic reticulum targeting sequence.

amino acids 219-222

N-glycosylation site.

amino acids 45-48

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 87-223, 129-142

EF-hand calcium-binding domain proteins

amino acids 202-214, 195-214

FIGURE 105

CAGAA**ATG**CAGGGACCATTGCTTCTTCCAGGCCTCTGCTTGCTGAGCCTTTGGAGCT
GTGACTCAGAAAACCAAAACTTCCTGTGCTAAGTGCCCCCAAATGCTCCTGTGTCAATAA
CACTCACTGCACCTGCAACCATGGATATACTTCTGGATCTGGGAGAAACTATTCACATTCC
CCTTGGAGACATGTAACGCCAGGCATGGTGGCTCGCGCCTG**TAA**TCCCAGTTCTTGGGAAG
CCAAGGCAGGTGGATCACCTGAGGTCAAGGAGTTGAGACCAGCCTGCCAACATAGTGAACAC
CCCGTGTCTACTAAAAATACAAAAATCAGCCGGCGTGGTGGTGCATGCCTGCAATCCAGT
TACTCGGGAGGCTGAGGCAGGAGAATCGCTGAACTCAGGAGGCAGAAGTTGCAGTGAACCC
AGATCCTGCCATTGCACTCCAGCATGGATGACAGAGCAAGACTCCGTCTAAAAAGAAAAGA
TAGTTCTTGTTCATTCGCGACTGCCCTCTCAGTGTTCCTGGATCCCCTCCAAATAA
AGTACTTATATTCTC

FIGURE 106

MQGPLLLPGLCFLLSLFGAVTQKTKTSCAKCPPNASCVNNTHCTCNHGYTSGSGQKLFTFPL
ETCNARHGGSR

Signal peptide:

amino acids 1-18

FIGURE 107

CAAGCAGGT CATCCCCTGGT GACCTCAAAGAGAAGCAGAGAGGGCAGAGGTGGGGGCAC
AGGAAAGGGTGACCTCTGAGATTCCCCTTCCCCAGACTTGAAGTGACCCACC**ATGG**
GGCTCAGCATTTGCTCCTGTGTCTGGGCTAGCCAGGCAGCCACACCGAAGATT
TTCAATGGCACTGAGTGTGGCGTAACTCACAGCCGTGGCAGGTGGGCTGTTGAGGGCAC
CAGCCTGCGCTGCGGGGTGTCCTATTGACCACAGGTGGGCTCACAGCGGCTCACTGCA
GCGGCAGCAGGTACTGGTGCGCCTGGGGAACACAGCCTCAGCCAGCTCGACTGGACCGAG
CAGATCCGGCACAGCGGTTCTGTGACCCATCCCGCTACCTGGAGCCTCGACGAGCCA
CGAGCACGACCTCCGGCTGCTGCCCTGCCGTCCCGTAACCAGCAGCGTTCAAC
CCCTGCCCTGCCAATGACTGTGCAACCGCTGGCACCGAGTGCCACGTCTCAGGCTGGGGC
ATCACCAACCACCCACGGAACCCATTCCGGATCTGCTCCAGTGCCTAACCTCTCCATCGT
CTCCCATGCCACCTGCCATGGTGTATCCCGGAGAACATCACGAGCAACATGGTGTGCAG
GCGGCGTCCGGGGCAGGATGCCCTGCCAGGGTATTCTGGGGCCCTGGTGTGGGGGA
GTCCTCAAGGTCTGGTGCCTGGGGCTGTGGGCCCTGTGGACAAGATGGCATCCCTGG
AGTCTACACCTATTTGCAAGTATGTGGACTGGATCCGGATGATCATGAGGAACA**TGA**C
CTGTTCCACCTCCACCCACCCCTAACCTGGTACCCCTCTGGCCCTCAGAGCACC
AATATCTCCCATCACTCCCTAGCTCCACTCTGGCCTGGAACTTCTTGGAACTT
TAACTCCTGCCAGCCCTCTAAGACCCACGAGCGGGTGAGAGAAGTGTGCAATAGTCTGGA
ATAAATATAATGAAGGAGGGCAAAAAAAAAAAAAAA

FIGURE 108

MGLSIFLLLKVGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH
CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRVTSSV
QPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITSNMVC
AGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPGCGQDGIPGVYTYICKYVDWIRMMRNN

Signal peptide:

amino acids 1-17

FIGURE 109

GC GGCCACACGCAGCTAGCCGGAGCCCGGACCAGGCCTGTGCCTCCTCGTCCCTCGC
CGCGTCCCGAAGCCTGGAGCCGGGGAGCCCCCGCGCTGCC **ATG** CGGGCGAGCTCAGCA
ACAGGTTCCAAGGAGGGAAAGCGTTGGCTCAAAGCCCAGGAGAGGAGGCTGGC
GAGATCAACCGGGAGTTCTGTGTGACCAGAAGTACAGTGATGAAGAGAACCTTCAGAAAA
GCTCACAGCCTCAAAGAGAAGTACATGGAGTTGACCTGAACAATGAAGGCGAGATTGACC
TGATGTCTTAAAGAGGATGATGGAGAAGCTTGGTGTCCCCAAGACCCACCTGGAGATGAAG
AAGATGATCTCAGAGGTGACAGGAGGGTCAGTGACACTATATCCTACCGAGACTTGTGAA
CATGATGCTGGGAAACGGTCGGCTGCCTCAAAGTTAGTCATGATGTTGAAGGAAAAGCCA
ACGAGAGCAGCCCCAAGCCAGTTGGCCCCCTCCAGAGAGAGACATTGCTAGCCTGCC **TGA**
GGACCCCGCCTGGACTCCCCAGCCTCCCACCCATACCTCCCTCCGATCTGCTGCCCTT
CTTGACACACTGTGATCTCTCTCTCATTTGTTGGTCATTGAGGGTTGTTGTGTT
TCATCAATGTCTTGTAAAGCACAAATTATCTGCCTAAAGGGCTCTGGTCGGGAATCC
TGAGCCTTGGTCCCTCCCTCTCTTCTCCCTCCGCTCCGTGAGAAGGGCTG
ATATCAAACCAAAACTAGAGGGGGCAGGCCAGGGCAGGGAGGCTCCAGCCTGTGTTCCC
CTCACTTGGAGGAACCAGCACTCTCCATCCTTCAGAAAGTCTCCAAGCCAAGTTAGGCTC
ACTGACCTGGCTCTGACGAGGACCCAGGCCACTCTGAGAAGACCTTGGAGTAGGGACAAGG
CTGCAGGGCCTTTGGGTTCTGGACAGTGCATGGTCCAGTGCTCTGGTGTACCC
AGGACACAGCCACTCGGGGCCCGCTGCCAGCTGATCCCCACTCATTCCACACCTTTCT
CATCCTCAGTGATGTGAAGGTGGAAAGGAAAGGAGCTTGGCATTGGAGCCCTCAAGAAGG
TACCAGAAGGAACCCTCCAGTCCTGCTCTGCCACACCTGTGCAGGCAGCTGAGAGGCAG
CGTGCAGCCCTACTGCTTACTGGGCAGCAGAGGGCTCGGAGGCAGAAGTGAGGCCTG
GGTTTGGGGAAAGGTCAAGTCAGTGCTGTTCCACCTTTAGGGAGGATACTGAGGGGAC
CAGGATGGAGAATGAGGAGTAAATGCTCACGGCAAAGTCAGCAGCACTGGTAAGCCAAGA
CTGAGAAATACAAGGTTGCTGTGACCCCAATCTGCTGAAAAAAAAAAAAAA

FIGURE 110

MSGELSNRFQGGKAFGLLKARQERRLAEINREFLCDQKYSDEENLPEKLTA
FKEKYMEFDLN
NEGEIDLMSLKRMMEKLGVPKTHLEMKKMISEVTGGVSDTISYRDFVNMM
MLGKRSAVLKLVM
MFEKGKANESSPKPVGPPP
ERDIASLP

Y₁ Y₂ Y₃ Y₄ Y₅ Y₆ Y₇ Y₈ Y₉ Y₁₀ Y₁₁ Y₁₂ Y₁₃ Y₁₄ Y₁₅ Y₁₆ Y₁₇ Y₁₈ Y₁₉ Y₂₀ Y₂₁ Y₂₂ Y₂₃ Y₂₄ Y₂₅ Y₂₆ Y₂₇ Y₂₈ Y₂₉ Y₃₀ Y₃₁ Y₃₂ Y₃₃ Y₃₄ Y₃₅ Y₃₆ Y₃₇ Y₃₈ Y₃₉ Y₄₀ Y₄₁ Y₄₂ Y₄₃ Y₄₄ Y₄₅ Y₄₆ Y₄₇ Y₄₈ Y₄₉ Y₅₀ Y₅₁ Y₅₂ Y₅₃ Y₅₄ Y₅₅ Y₅₆ Y₅₇ Y₅₈ Y₅₉ Y₆₀ Y₆₁ Y₆₂ Y₆₃ Y₆₄ Y₆₅ Y₆₆ Y₆₇ Y₆₈ Y₆₉ Y₇₀ Y₇₁ Y₇₂ Y₇₃ Y₇₄ Y₇₅ Y₇₆ Y₇₇ Y₇₈ Y₇₉ Y₈₀ Y₈₁ Y₈₂ Y₈₃ Y₈₄ Y₈₅ Y₈₆ Y₈₇ Y₈₈ Y₈₉ Y₉₀ Y₉₁ Y₉₂ Y₉₃ Y₉₄ Y₉₅ Y₉₆ Y₉₇ Y₉₈ Y₉₉ Y₁₀₀

FIGURE 111A

CGCGCTCCCCGCGCCCTCCTGGGCTCCACGCGTCTGCCCGCAGAGGCAGCCTCTCCA
 GGAGCGGGGCCCTGCACACCATGGCCCGGGGTGGCAGGGGTGGCGCCGCGCC
 CGCTGGCGCTGGCCTGGCGCTGGCGAGCGTCTGAGTGGGCTCCAGCGTCGCTGCC
 CACCAAGTGTACCTGCTCCGCTGCCAGCGTGGACTGCCACGGCTGGCCTCCGCGGGTTC
 CTCGGGCATCCCCGCAACGCTGAGCGCTTGACCTGGACAGAAATAATACCAAGGATC
 ACCAAGATGGACTTCGCTGGCTCAAGAACCTCGAGTCTGCATCTGAAGACAACCAGGT
 CAGCGTCATCGAGAGAGGGCGCTTCCAGGACCTGAAGCAGCTAGAGCAGTCGCGCTGAACA
 AGAATAAGCTGCAAGTCCTCCAGAATTGCTTCCAGAGCACGCCGAAGCTCACCAGACTA
 GATTGAGTGAAAACCAGATCCAGGGATCCCAGGAAGGGCTCCGCGGCATACCGATGT
 GAAGAACCTGCAACTGGACAACAACCACATCAGCTGCATTGAAGATGGAGCCTCCGAGCGC
 TCGCGATTGGAGATCCTAACCTAACAAACAAACATCAGTCGATCTGGTACCGAGC
 TTCAACCACATGCCAAGATCCGAACTCTGCGCCTCCACTCCAACCACCTTAACCGACTG
 CCACCTGGCCTGGCTCTCGGATTGGCTGCGACAGCAGGACAGTTGCCAGTCACACTCT
 GCATGGCTCTGTGCATTGAGGGCTTCAACGTGGCGATGTGCGAGAAGAAGGAGTACGTG
 TGCCCAGCCCCCCTCGGAGCCCCCATCCTGCAATGCCACTCCATCTCTGCCCTCGCC
 CTGACGTGCAGCAATAACATCGTGGACTGTGAGGAAAGGGCTTGATGGAGATTCTGCCA
 ACTTGCCGGAGGGCATCGTCAAATACGCCTAGAACAGAACTCCATCAAAGCCATCCCTGCA
 GGAGCCTCACCCAGTACAAGAAACTGAAGCGAATAGACATCAGCAAGAATCAGATATCGGA
 TATTGCTCCAGATGCCCTCCAGGGCTGAAATCACTCACATCGTGGTCTGTATGGAAACA
 AGATCACCGAGATTGCAAGGGACTGTTGATGGGCTGGTCCCTACAGCTGCTCTCCTC
 AATGCCAACAGATCAACTGCCCTGCGGGTAACACGTTCAAGGACCTGCAAGAACCTCAACTT
 GCTCTCCCTGTATGACAACAAGCTGCAAGGACATCAGCAAGGGCTTCTGCCCTCTGCACT
 CCATCCAGACACTCCACTTAGCCCCAAACCCATTGTTGCGACTGCCACTTGAAGTGGCTG
 GCCGACTACCTCCAGGACAACCCCCATCGAGACAAGCGGGGCCGCTGCAGCAGCCCGCCG
 ACTCGCCAACAAGCGCATCGCCAGATCAAGAGCAAGAAGTCCGCTGCTCAGGCTCCGAGG
 ATTACCGCAGCAGGTTCAAGCAGCGAGTGCTCATGGACCTCGTGTGCCCCGAGAAGTGTGCG
 TGTGAGGGCACGATGTGGACTGCTCAACCAGAAGCTGGTCCGATCCAAAGCCACCTCCC
 TGAATATGTCACCGACCTGCGACTGAATGACAATGAGGTATCTGTTCTGGAGGCCACTGGCA
 TCTTCAAGAAGTTGCCAACCTGCGAAAATAATCTGAGTAACAATAAGATCAAGGAGGTG
 CGAGAGGGAGCTTCGATGGAGCAGCAGCGTGCAGGAGCTGATGCTGACAGGGAACCAGCT
 GGAGACCGTGCACGGCGCGTTCGGCTCAGTGGCTCAAACCTTGATGCTGAGGA
 GTAACTTGATCAGCTGTGAGTAATGACACCTTGCCGGCTGAGTTGGTGGAGACTGCTG
 TCCCTCTATGACAATCGGATCACCACCATCACCCTGGGGCTTCACCACGCTTGTCTCCCT
 GTCCACCATAAACCTCTGTTCAACCCCTCACTGCAACTGCCACCTGGCCTGGCTCGGCA
 AGTGGTTGAGGAAGAGGCGGATCGTCAGTGGAAACCTAGGTGCCAGAAGCCATTTCCTC
 AAGGAGATCCCACCCAGGATGTGGCATCCAGGACTTCACCTGTGATGGCAACGAGGAGAG
 TAGCTGCCAGCTGAGCCCCGCGTGCCTGGAGCGAGTGCACCTGTATGGAGACAGTGGTGC
 GCAGCAACAAGGGCTCCGCGCCCTCCCCAGAGGCATGCCAAGGATGTGACCGAGCTGTAC
 CTGGAAAGGAAACCACCTAACAGCGTGGCCAGAGAGAGCTGTCGCGCCCTCCGACACCTGACGCT
 TATTGACCTGAGCAACAACAGCATCAGCATGCTGACCAATTACACCTTCAGTAACATGTCTC
 ACCTCTCCACTCTGATCCTGAGCTACAACCGGCTGAGGTGCATCCCCGTCCAGCCCTCAAC
 GGGCTGCAGTCCCTGCGAGTCTAACCCATGGCAATGACATTCCAGCGTTCTGAAGG
 CTCCCTCAACGACCTCACATCTCTTCCCACATCTGGCGCTGGGAACCAACCCACTCCACTGTG
 ACTGCAGTCTCGGTGGCTGCGAGTGGGTGAAGGCAGGGTACAAGGAGCCTGGCATGCC
 CGCTGCAGTAGCCCTGAGCCCATGGCTGACAGGCTCCTGCTCACCACCCCAACCCACCGCTT
 CCAGTGCAGAAGGGCAGTGGACATCAACATTGTTGGCAAATGCAATGCCCTCCAGCC
 CGTGCAAGAATAACGGGACATGCACCCAGGACCCCTGTGGAGCTGTACCGCTGTGCCCTGCC

FIGURE 111B

TACAGCTACAAGGGCAAGGACTGCACTGTGCCCATCACACCTGCATCCAGAACCCCTGTCA
GCATGGAGGCACCTGCCACCTGAGTGACAGCCACAAGGATGGGTTAGCTGCTCTGCCCTC
TGGGCTTGAGGGGCAGCGGTGTGAGATCAACCCAGATGACTGTGAGGACAACGACTGCGAA
AACAAATGCCACCTGCGTGGACGGATCAACAACACTACGTGTATCTGTCGGCTAACTACAC
AGGTGAGCTATGCGACGAGGTGATTGACCACTGTGTGCCAGCTGAACCTCTGTCAGCATG
AGGCCAAGTGCATCCCCCTGGACAAAGGATTAGCTGCGAGTGTGCCCTGGCTACAGCGGG
AAGCTCTGTGAGACAGACAATGATGACTGTGTGGCCCACAAGTGCCGCCACGGGGCCAGTG
CGTGGACACAATCAATGGCTACACATGCACCTGCCCTCAGGGCTTCAGTGGACCCCTGTG
AACACCCCCCACCACATGGCTCTACTGCAGACCAGCCCAGCAGCTGCGACCAGTACGAGTGC
GGGGCCCAGTGCATCGTGGTGCAGCAGGAGCCCACCTGCCGCTGCCACCAGGCTTCGCCGG
CCCCAGATGCGAGAAGCTCATCACTGTCAACTTCGTGGCAAAGACTCCTACGTGGAAC
CCTCCGCCAAGGTCCGACCCCAGGCCAACATCTCCCTGCAGGTGGCCACTGACAAGGACAAC
GGCATCCTCTCTACAAAGGAGACAATGACCCCCCTGGCACTGGAGCTGTACCAAGGGCAC
GCGGCTGGTCTATGACAGCCTGAGTTCCCTCCAACCACAGTGTACAGTGTGGAGACAGTGA
ATGATGGCAGTTCACAGTGTGGAGCTGGTACGCTAAACACAGACCCCTGAACCTAGTAGTG
GACAAAGGAACCTCAAAGAGCCTGGGAAGCTCCAGAAGCAGCCAGCAGTGGCATCAACAG
CCCCCTCTACCTTGGAGGCATCCCCACCTCCACCAGGCTTCCGCTGCGCCAGGGCACGG
ACCGGCTCTAGGCGGCTTCCACGGATGCATCCATGAGGTGCGCATCAACAAGGAGCTG
GACTTCAAGGCCCTCCACACAGTCCCTGGGGTGTCAACCAGGCTGCAAGTCTGCACCGT
GTGCAAGCACGGCCTGTGCCGCTCCGTGGAGAAGGACAGCGTGGTGTGCGAGTGC
GCTGGACCGGCCACTCTGCGACCAAGGAGGCCGGACCCCTGCCTCGGCCACAGATGCCAC
CATGGAAAATGTGTGGCAACTGGGACCTCATACATGTGCAAGTGTGCCAGGGCTATGGAGG
GGACTTGTGTGACAACAAGAATGACTCTGCCATGCCGCTCAGCCTCAAGTGTCAACCATG
GGCAGTGCCACATCTCAGACCAAGGGGAGCCCTACTGCCGTGCCAGCCGGCTTAGGGC
GAGCACTGCCACAAAGAGAATCCGTGCCGGACAAGTAGTCCGAGAGGTGATCCGCC
GAAAGGTTATGCATCATGTGCCACAGCCTCAAGGTGCCCATCATGGAATGTG
GTGGGGCCCCAGTGTGCCAGCCACCCGCAGCAAGGGGGAAATACGTCTTCAGTGCACG
GACGGCTCTCGTTGTAGAAGAGGTGGAGAGACACTTAGAGTGC
TAAGGCCCTGCCGCCCTGCCACCTCTCGGACTCCAGCTTGATGGAGTTGGGACAGCC
ATGTGGGACCCCTGGTATTGACATGAAGGAAATGAAGCTGGAGAGGAAGGTAAAGAAGA
AGAGAATATTAAGTATATTGAAACAAAAAATAGAACTTAAAAAAAAAAAAAAA
AAAAAA

FIGURE 112

MAPGWAGVGA AVR LAL ALA SVL SGPP AVAC PT KCTCSA ASVD CHGL GLRA VPRG I PRN
 AER LD LDR NNITR IT KMD FAG LKNL RVL HLED NQV SIER GA FQDL KQL ER LRL NKNK LQVL
 PELL FQST PKL TRL DLS EN QI QGIP RKA FRG IT DV KNL QLD NNH ISC IED GAF RA LRD LEIL
 TI NNNN IS RIL VTS FN HMP KIR TL RL HS NH LY CD CH LA WL SD WLR QR RT VG QFT LC MAP VHL
 RGF NVAD VQ KKEY VCP APH SE PP SC NANS IS CP SP CT CS NN IV DC RGK GL ME I PAN LPEG IV
 EIR LEQ NSI KA I PAGA FT QY KKL KRI DIS K NQ I S DI AP DA FQ GL KSL TSL VLY GN KITE IA K
 GL FD GL VSL QLLL NANK IN CL RV NT FQ DL QN LN LL S IY DN K LQ TIS K GL FAP LQ SI QT LHL
 A QN P FV C DCH LK WLA DYL QDN PI ET SG AR CS S P RRL AN K RIS QI K SKK FRC SG S E DY RS RF S
 SEC FMD LVC PE K CRCE GT IV DC SN QK LV RI PSH LPE YV TD RL ND NE VS VLE AT G IF KK LP N
 LR KIN LS NN KI KE VREG A FD G A AS VQ EMLT GN QLET VH GRV FR GL SG LK TLM LRS NL I SC V
 SND TFA GL SS VR LL S IY DN RITT IT PG AFT T L VSL STI NLL S NP FNC NC HLA WL GK WLR KRR
 IV SGN PRC QK PFF LKE IPI QD VAI QD FT CD GNE ESSC QL S PRC P E QCT CMET VV RC SN K GL R
 AL PR GM PKD VTE LY LEG NHT A VPRE LSA RL HT LID L SNN S I SML TN YTF SN MSH LST LIL
 SY NR LRC I PV HAF NGL RSL RV LT LH GND I SS VPE GS FND L TS L SH L AL GT NPL HCD C SL RW L
 SE WVK AGY KEP G IAR CS S P E PM A DR L LTT PTH FQ CK GP VD IN I VAK CNA CL S PCK NNG T
 CT QDP VEL YRC AC PYS YKG K DCT V PINT CI QN PC QH GGT CH LSD SH KDG FSC SC PLG FEG Q R
 CE I NPD D CED ND CEN NAT CVD GIN NY V CIC P PNY TGE LC D E V ID HCV P E L NLC QHE AK C I PL
 DK GF S CEC VPG YSG KLC ET D N DDC VAH KCR HG AQC VDT IN GYT CT CP QGF SG F C E H P PPM V
 LL QTSP CD QYE C QNG AQC I VV QQE PTC RCP PGF AGP RCE K LIT VNF VG KDS Y VEL ASAK V RP
 QAN ISL QV AT D K DNG ILL YKG DND P L A L E LY QGH VRL VY DS LSS PTT VY S VET VND GQ FHS
 VEL VTL NQ TL NL VV DKG TP KSL GKL QK QPAVG I NS PLY LGGI PT ST GLS AL RQ GT DRPL GGF
 HG CI HE VR IN NEL QDF K AL PP QSL GV SP GCK S CT VCK HGL CRS VE KDS VV C E R P GWT GPL C
 DQE ARD PCL GHR CH HGK CV AT GT SY MCK CAEG YGG D L C DN K ND SAN A C SA FK CH H GQ CH I SD
 QGE PY CLC QPG FSG E HC Q QEN PCL GQ VV RE V IR RQ KG YAS C AT ASK V PIM E CR GG CG P QCC Q
 PTR SK RR KY V FQ CT DG SS F VEE EVER HLE CG CL ACS

Signal peptide:

amino acids 1-27

FIGURE 113

GGATGCAGGACGCTCCCTGAGCTGCCTGTACCGACTAGGTGGAGCAGTGTTCCTCCGCA
GACTCAACTGAGAAGTCAGCCTCTGGGGCAGGCACCAGGAATCTGCCTTCAGTTCTGTCT
CCGGCAGGCTTGAGGAATGAAGGCTGCCGCATTCTGACCCCTCATTGGCTGCCTGGTCACAG
GCGCCGAGTCCAAAATCTACACTCGTTGCAAACGGCAAAATATTCTCGAGGGCTGGCCTG
GACAATTACTGGGCTTCAGCCTGGAAACTGGATCTGCATGGCATATTATGAGAGCGGCTA
AACACACCACAGCCCCGACGGCCTGGATGACGGCAGCAGTCACTATGGCATCTTCCAGATCA
ACAGCTTCGGTGGTGCAGACCGGAAAGCTGAAGGAGAACACCAACTGCCATGTCGCCTGC
TCAGCCTTGATCACTGATGACCTCACAGATGCAATTATCTGTGCCAGGAAAATTGTTAAAGA
GACACAAGGAATGAACATTGGCAAGGCTGGAAGAAACATTGTGAGGGCAGAGACCTGTCCG
AGTGGAAAAAAAGGCTGTGAGGTTCCTAAACTGGAACGGACCCAGGATGCTTGCAGCAAC
GCCCTAGGATTGCACTGAATGTCAAATGCCGTGTGCATCTGTCCCCTCCAAATA
TTCCTTCTCAAACCTGGAGAGGGAAAATTAGCTATACTTTAAGAAAATAATTTCCAT
TTAAATGTC

FIGURE 114

MKAAGILTTLIGCLVTGAESKIKYTRCKLAKIFSRAGLDNYWGFSLGNWICMAYYESGYNTTAP
TVLDDGSIDYGIFQINSFAWCRRGKLKENNHCHVACSAITDDLTDAAICARKIVKETQGMN
YWQGWKKHCEGRDLSEWKKGCEVS

Signal peptide:

amino acids 1-19

FIGURE 115

CAGGCCATTGCATCCCACTGTCCTGTGGAGGCCAGGCCACACCGTCCTCAGCAGTGT
 CATGTGTTAAAAACGCCAAGCTGAATATATC**ATG**CCCCTATTAAAACCTTGATACATGGCTCCC
 CATTGGTTTGAGAAAAGTTCAAGCTTTACCTGGTGTGCCTGTATCCCAGTGTTC
 AGGCTGGCTAGACGGCGGAAGAAGATCCTATTTACTGTCACTTCCCAGATCTGCTCTCAC
 CAAGAGAGATTCTTCTAAACGACTATAACAGGGCCCCATTGACTGGATAGAGGAATACA
 CCACAGGCATGGCAGACTGCATCTTAGTCAACAGCCAGTCACAGCTGCTTTAAGGAA
 ACATTCAAGTCCCTGTCTCACATAGACCCTGATGTCCTCTATCCATCTAAATGTCAACCAG
 CTTGACTCAGTTGTCCTGAAAAGCTGGATGACCTAGTCCCCAAGGGAAAAAATCCTGC
 TGCTCTCCATCAACAGATA CGAAAGGAAGAAAAATCTGACTTTGGCACTGGAAGCCCTAGTA
 CAGCTGCGTGGAGATTGACATCCCAAGATTGGAGAGGGTTCATCTGATCGTGGCAGGTGG
 TTATGACGAGAGAGTCCTGGAGATGTGGAACATTATCAGGAATTGAAGAAAATGGTCCAAC
 AGTCCGACCTTGGCCAGTATGTGACCTTCTTGAGGTCTTCTCAGACAAACAGAAAATCTCC
 CTCCTCCACAGCTGCACGTGTGCTTACACACCAAGCAATGAGCACTTGGCATTGTCCC
 TCTGGAAGCCATGTACATGCAGTGCCAGTCATTGCTGTTAATTGGTGGACCCTGGAGT
 CCATTGACCACAGTGTACAGGGTTCTGTGAGCCTGACCCGGTGCACCTCTCAGAAGCA
 ATAGAAAAGTTCATCCGTGAACCTCCTAAAAGCCACCATGGGCTGGCTGGAAGAGCCAG
 AGTGAAGGAAAATTTCCCTGAAGCATTACAGAACAGCTCTACCGATATGTTACCAAAC
 TGCTGGT**TAA**TCAGATTGTTAAGATCTCCATTAATGTCATTTTATGGATTGTAGACC
 CAGTTTGAAACCAAAAAGAACCTAGAATCTAATGCAGAAGAGATCTTAAAAAATAAA
 CTTGAGTCTGAATGTGAGCCACTTCTATACACACCTCCGTCCACTTTCAAGAAA
 AACCATGTTATGCTATAATCATTCCAAATTGGCCAGTGTAAAGTTACAAATGTGGTG
 TCATTCCATGTTAGCAGAGTATTAAATTATTTCTGGGATTATTGCTCTGTCTA
 TAAATTGAAATGATACTGTGCCTAATTGGTTTCAAGTTAAGTGTATCATTATCAA
 AGTTGATTAATTGGCTTCAAGTATAATGAGAGCAGGGCTATTGTAGTCCCAGATTCAAT
 CCACCGAAGTGTCACTGTCATCTGTTAGGAAATTGGTGTCTGTCTGGATC
 CATAGCGAGAGTGCTCTGTATTTTAAGATAATTGTATTTGCACACTGAGATATAA
 TAAAAGGTGTTATCATAAAAAAAAAAAAAAA

FIGURE 116

MPLLKLVHGSPLVGEFKLFTLVSACIPVFRLLARRKKILFYCHFPDLTTKRDSDLKRLY
RAPIDWIEEYTTGMADCILVNSQFTAAVFKETFKSLSHIDPDVLYPSLNVTSDSVVPEKLD
DLVPKGKKFLLSINRYERKKNLTLALEALVQLRGRLTSQDWERVHLIVAGGYDERVLENVE
HYQELKKMVQQSDLGQYVTFLRSFSDKQKISLLHSCTCVLYTPSNEHFGIVPLEAMYMQCPV
IAVNSGGPLESIDHSVTGFLCEPDPVHFSEAIKEFIREPSLKATMGLAGRARVKEKFSPEAF
TEQLYRYVTKLLV

Signal peptide:

amino acids 1-15

FIGURE 117

GACTACGCCGATCCGAGACGTGGCTCCCTGGCGGCAGAACCAATGTTGGACTTCGCGATCTT
 CGCCGTTACCTTCTGCTGGCGTTGGTGGAGCCGTGCTTACCTCTATCCGGCTTCCAGAC
 AAGCTGCAGGAATTCCAGGGATTACTCCAAGTGAAGAAAAAGATGGTAATCTTCCAGATATT
 GTGAATAGTGGAAAGTTGCATGAGTTCTGGTTAATTTGCATGAGAGATATGGCCTGTGGT
 CTCCTCTGGTTGGCAGGCGCCTCGTGGTTAGTTGGCACTGTTGATGTACTGAAGCAGC
 ATATCAATCCAATAAGACATCGGACCCTTGAAACCATGCTGAAGTCATTATTAAGGTAT
 CAATCTGGTGGCAGTGTGACTGAAAACCACATGAGGAAAAATTGTATGAAAATGGTGT
 GACTGATTCTCTGAAGAGTAACCTTGCCCTCCTAAAGCTTCAGAAGAATTATTAGATA
 AATGGCTCTCCTACCCAGAGACCCAGCACGTGCCCTCAGCCAGCATATGCTTGGTTTGCT
 ATGAAGTCTGTTACACAGATGGTAATGGTAGTACATTGAAGATGATCAGGAAGTCATTG
 CTTCCAGAAGAACATGGCACAGTTGGTCTGAGATTGGAAAAGGCTTCAGATGGTCAC
 TTGATAAAAACATGACTCGGAAAAACAATATGAAGATGCCCTCATGCAACTGGAGTCTGTT
 TTAAGGAACATCATAAAAGAACGAAAAGGAAGGAACCTCAGTCAACATATTCATTGACTC
 CTTAGTACAAGGAAACCTTAATGACCAACAGATCCTAGAACAGACTATGATATTTCTCTGG
 CCAGTTGCATAATAACTGCAAAATTGTGTACCTGGCAATCTGTTTTAACCACCTCTGAA
 GAAGTTCAAAAAAAATTATATGAAGAGATAAACCAAGTTGGAAATGGCCTGTACTCC
 AGAGAAAATTGAGCAGCTCAGATATTGTCAGCATGTGCTTGTGAAACTGTTGAACTGCCA
 AACTGACTCCAGTTCTGCCAGCTCAAGATATTGAAGGAAAATTGACCGATTATTATT
 CCTAGAGAGACCCCTCGCCTTATGCCCTGGTGTGGTACTTCAGGATCTAACACTGGCC
 ATCTCCACACAAGTTGATCCAGATCGGTTGATGATGAATTAGTAATGAAAACCTTCC
 CACTTGGATTCTCAGGCACACAGGAGTGTCCAGAGTTGAGGTTGCATATATGGTGA
 GTACTTCTTAGTGTATTGGTGAAGAGACTGCACCTACTTCTGAGGGACAGGTTATTGA
 AACAAAGTATGAACTGGTAACATCATCAAGGGAAGAACGCTTGGATCACTGCTCAAAGAGAT
 ATTAAAATTTATACATTAAAATCATTGTTAAATTGATTGAGGAAAACAACCATTAAAAA
 AAATCTATGTTGAATCCTTTATAAACCAAGTATCACTTGTAAATATAAACACCTATTGTAC
 TTAA

FIGURE 118

MLDFAIFAVTFLLALVGAVLYLYPASRQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLH
ERYGPVVFWFGRRLVVSLGTVDVLKQHINPNKTSDPFETMLKSILLRYQSGGGSVSENHMRK
KLYENGVTDSLKSNFALLLKSEELLDKWLSYPETQHVPLSQHMLGFAMKSVTQMVMGSTFE
DDQEVIREFQKNHGTVWSEIGKGFLDGSLDKNMTRKKQYEDALMQLESVLRNIIKERKGRNFS
QHIFIDSLVQGNLNDQQILEDSMIFSLASCIITAKLCTWAICFLTTSEEVQKKLYEEINQVF
GNGPVTPEKIEQLRYCQHVL CETVRTAKLTPVSAQLQDIEGKIDRFIIIPRETLVLYALGVVL
QDPNTWPSPHKFDPDRFDELVMKT FSSLGFSGTQECPELRFAYMVT TVLLSVLVKRLHLLS
VEGQVIETKYELVTSSREEAWITVSKRY

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 271-290

FIGURE 119

CTAGATTGTCGGCTTGCAGGGAGACTTCAGGAGTCGCTGTCTGAACCTCCAGCCTCAGA
GACCGCCGCCCTTGTCCCCGAGGGC**ATG**GGCCGGGTCTCAGGGCTTGTGCCCTCTCGCTTC
CTGACGCTCCTGGCGCATCTGGTGGTCGTACACCTTATTCTGGTCCCAGGACAGAACAT
ACAGGCCTGCCTGCCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATTCAAGCTGG
TGGCCGCGCTCTGTACCCCTGGGCCTTTGCAGTGGAGCTGGCCGGTTCTCAGGA
GTCTCCATGTTAACAGCACCCAGAGCCTCATCTCCATTGGGCTCACTGTAGTGCATCCGT
GGCCCTGTCCCTTCTCATATTGAGCGTTGGAGTGCACTAGTATTGGTACATTTTGCT
TCTGCAGTGCCCTTCCAGCTGTCAGTGAAATGGCTTATTGTCACCGTCTTGGGCTGAAA
AAGAAACCCTTC**TGA**TTACCTCATGACGGAACCTAACGGACGAAGCCTACAGGGCAAGGG
CCGCTTCGTATTCCCTGGAAGAAGGAAGGCATAGGCTTCGGTTTCCCCTGGAAACTGCTTC
TGCTGGAGGATATGTGTTGAAATAATTACGTCTTGAGTCTGGATTATCCGCATTGTATTAA
GTGCTTGTAAATAAAATGTTTAGTAACATTAAGACTTATACAGTTTAGGGACA
ATTAAAAAAA

FIGURE 120

MGRVSGLVPSRFLTLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLG
LFAVELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCSALPAVT
EMALFVTVFGLKKKPF

Transmembrane domain:

amino acids 12-28 (type II), 51-66, 107-124

FIGURE 121

TCCCGGACCCTGCCGCCCTGCCACTATGTCCC GCC GCT CTATGCTGCTTG CCTGGG CTCTCC
CCAGCCTCCTCGACTCGGAGCGGCTCAGGAGACAGAAGACCCGGCCTGCCTGCAGCCCCATA
GTGCCCGGAACGAGTGGAAAGGCCCTGGCATCAGAGTGC GCCCAGCACCTGAGCCTGCCCTT
ACGCTATGTGGTGGTATCGCACACGGCGGGCAGCAGCTGCAACACCCCCGCCCTCGTGCCAGC
AGCAGGCCCGGAATGTGCAGCACTACCACATGAAGACACTGGGCTGGTGCACGTGGCTAC
AACTT CCGATTGGAGAAGACGGGCTCGTATACGAGGGCCGTGGCTGGAACCTCACGGGTGC
CCACTCAGGTCACTTATGGAACCCATGTCCATTGGCATCAGCTTCATGGCAACTACATGG
ATCGGGTGCCCACACCCAGGCCATCGGGCAGCCCAGGGTCTACTGGCCTGCGGTGTGGCT
CAGGGAGCCCTGAGGTCCA ACTATGTGCTCAAAGGACACCGGGATGTGCAGCGTACACTCTC
TCCAGGCAACCAGCTCTACCACCTCATCCAGAATTGCCACACTACCGCTCCCCTGAGGCC
CTGCTGATCCGCACCCATTCCCTCCCATGGCAAAAACCCC ACTGTCTCCTTCTCCA
ATAAAGATGTAGCTC

FIGURE 122

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHT
AGSSCNTPASCQQQARNVQHYHMKTGLWCDVGYNFLIGEDGLVYERGWNTGAHSGLWNP
MSIGISFMGNYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHL
IQNWPHYRSP

Signal peptide:

amino acids 1-20

FIGURE 123

CTGGGACCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAG**ATG**CAACT
 GACTCGCTGCTGTTCTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGG
 ATGATGGTCCTCCGGCTCAGAGGACCTGAGCGTATGACCACGAGGCCAGCCCCGGCCC
 CGGGTGCCTCGGAAGCGGGGCCACATCTCACCTAACGTCAGTCCCGCCATTGGCCAATTCCACTCT
 CCTAGGGCTGCTGGCCCCGCCTGGGGAGGCTTGGGCATTCTTGGCAGCCCCCAACCGCC
 CGAACACAGCCCCCACCCTCAGCCAAGGTGAAGAAATCTTGGCTGGCGACTTCTAC
 TCCAACATCAAGACGGTGGCCCTGAACCTGCTCGTCACAGGAAGATTGTGGACCATGGCAA
 TGGGACCTTCAGCGTCCACTTCAACACAATGCCACAGGCCAGGAAACATCTCCATCAGCC
 TCGTCCCCCAGTAAAGCTGTAGAGTTCCACCAGGAACAGCAGATCTCATCGAAGCCAAG
 GCCTCCAAAATCTTCAACTGCCGGATGGAGTGGAGAAGGTAGAACGGGCCGCCGACCTC
 GCTTGACCCACGACCCAGCCAAGATCTGCTCCGAGACCACGCTCAGAGCTCAGCCACCT
 GGAGCTGCTCCCAGCCCTCAAAGTCGTCTGTCTACATGCCCTTACAGCACGGACTAT
 CGGCTGGTCCAGAAGGTGTGCCAGATTACAACATACCATAGTGTACCCCCCTACTACCCATC
 TGGG**TGA**CCCAGGGCAGGCCACAGAGGCCAGGGCTGGAAGGACAGGCCTGCCATGC
 AGGAGACCATCTGGACACCAGGGCAGGGAAAGGGGTTGGGCTCAGGCAGGGAGGGGGTGGAG
 ACGAGGAGATGCCAAGTGGGCCAGGCCAAGTCTCAAGTGGCAGAGAAAGGTCCAAGTG
 CTGGTCCCAACCTGAAGCTGTGGAGTGAATCACAGGAGCAGTGGAGGAGGAGTGGCT
 CTCTGTGCAGCCTCACAGGGCTTGCCACGGAGCCACAGAGAGATGCTGGGTCCCCGAGGCC
 TGTGGCAGGCCGATCAGTGTGGCCCAGATCAAGTCATGGAGGAAGCTAACGCCCTGGTT
 CTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGAGATTTCATCAGTGTGGACAGCCTG
 TCAACTTAGGATGGATGGCTGAGAGGGCTTCTAGGAGGCCAGTCAGCAGGGTGGGTGGGCC
 CAGAGGAGCTCTCAGCCCTGCCTAGTGGCGCCCTGAGCCCTTGTGCTGCTGAGCATG
 GCATGAGGCTGAAGTGGCAACCCTGGGTCTTGATGTCTTGACAGATTGACCATCTGTCTC
 CAGCCAGGCCACCCCTTCCAAAATCCCTCTGCCAGTACTCCCCCTGTACCAACCCATT
 GCTGATGGCACACCCATCCTAACGCTAACAGACAGGACGATTGTGGCCTCCACACTAACGCC
 ACAGCCCACCCATCCCGGTGCTGTGTCCCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAG
 CATCCATGTCCCAGAGGGGTCCTCAACAGTCAGCCTCACCTGTACGACCCGGGTTCTCC
 CGGATCTGGATGGCGCCGCCCTCTCAGCAGCGGGCACGGTGGGCGGGGCCGGCGCAGA
 GCATGTGCTGGATCTGTTCTGTGTCTGTCTGTGGGTGGGGAGGGAGGGAAAGTCTTGT
 GAAACCGCTGATTGCTGACTTTGTGTGAAGAATCGTGTCTTGGAGCAGGAAATAAGCTT
 GCCCGGGGCA

FIGURE 124

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521
><subunit 1 of 1, 252 aa, 1 stop
><MW: 28127, pI: 8.91, NX(S/T): 5
MQLTRCCFVFLVQGSLYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMAN
STLLGLLAPPGEAWGILGQPPNRPNHSPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVD
HGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMEWEKVERGR
RTSLCTHDPAKICSRDHAQSSATWSCSQPKVVCVYIAFYSTDYRLVQKVCPDYNHSDTPY
YPSG
```

Important features of the protein:

Signal peptide:

amino acids 1-14

N-glycosylation sites.

amino acids 62-65, 127-130, 137-140, 143-146

2-oxo acid dehydrogenases acyltransferase

amino acids 61-71

FIGURE 125

GTGAATGTGAGGGTTGATGACTTCAGATGTCTAGGAACCAGAGTGGGTGCAGGGGCCCA
 GGCAGGGCTGATTCTGGCGGAGGAGACTAGGGTAAAGGGTCTGCATGAGCTCCTTAAAG
 GACAAAGGTAAACAGAGCCAGCGAGAGAGCTCGAGGGAGACTTGTACTCAAGCCACAGAAT
 TGGTGGAAAGTGTGCGGCCGCCGCCGTCGCTCCTGCAGCGCTGTCGACCTAGCCGCTAG
 CATCTTCCCAGCACCGGGATCCCAGGGTAGGAGGCGACGCCGGCGAGCACCGGCCAGCC
 GGCTGCGCTGCCACACGGCTCACC**ATG**GGCTCCGGCGCCGGCGCTGTCGCGGTGCCG
 GCCGTGCTGCTGGTCTCACGCTGCCGGGCTGCCGTCTGGCACAGAACGACACGGAGCC
 CATCGTGTGGAGGGCAAGTGTCTGGTGGTGTGCGACTCGAACCCGGCACGGACTCCAAGG
 GCTCCTCTCCTCCCCGCTGGGATATCGGTCCGGCGGCCAACCTCAAGGTGCCCTCTCG
 GCGGTGCGGAGCACCAACCACGAGCCATCCGAGATGAGCAACAAGACGCGCATCTTACTT
 CGATCAGATCCTGGTGAATGTGGTAATTTTACATTGGAGTCTGTCTTGACACCAA
 GAAAAGGAATTACAGTTCAGTTCACGTGATTAAAGTCTACCAGAGCCAAACTATCCAG
 GTTAACTTGATGTTAAATGGAAAACCAGTAATATCTGCCCTTGCGGGGACAAAGATGTTAC
 TCGTGAAGCTGCCACGAATGGTGTCTGCTCACCTAGATAAAGAGGATAAGGTTACCTAA
 AACTGGAGAAAGGTAATTGGTTGGAGGCTGGCAGTATTCCACGTTCTGGCTTCTGGT
 TTCCCCCTA**TAG**GATTCAATTCTCCATGATGTTCATCCAGGTGAGGGATGACCCACTCCTG
 AGTTATTGGAAGATCATTTCATCATTGGATTGATGTTCTGGTTCTCATGGGTG
 GATATGGATTCTAAGGATTCTAGCCTGTCTGAACCAATACAAAATTCACAGATTATTGTG
 TGTGTCTGTTCACTATTTGGATTGGACTCTAACAGATAATACCTATGCTAAATGTA
 ACAGTCAAAAGCTGCTGCAAGACTTATTCTGAATTTCATTCCTGGATTACTGAATTAGT
 TACAGATGTGGAATTATTGTTAGTTAAAAGACTGGCAACCAGGTCTAAGGATTAGA
 AAACTCTAAAGTTCTGACTTCATCAACGGTTAGTGTGATACTGCCAAAGAACTGTATACTG
 TGTTAATATATTGATTATTTGTTTATTCTCTGGATTAGTTGTTGGTTCTGTAA
 AAAACTGGATTTTTTCAGTACTGGTATTATGTTCTCTAAAATAAGGTAATGAA
 TGGCTGCCACAAATTACCTGACTACGATATCATCGACATGACTCTCTCAAAAAAAA
 GAATGCTCATAGTGTATTAAATTGTATATGTGAAAGAGTCATATTCCAAGTTATATT
 TTCTAAGAAGAAGAATAGATCATAATCTGACAAGGAAAAGTTGCTTACCCAAATCTAAG
 TGCTCAATCCCTGAGCCTCAGCAAAACAGCTCCCGAGGGAAATCTTACCTTATTGC
 TCAACTTAATTAAAATGATTGATAATAACCACCTTATTAAAAACCTAACGGTTTTTT
 TCCGTAGACATGACCACTTATTAAACTGGTGGGGATGCTGTTCTAACCTTAAATTACCTAT
 TTTCAAGGCTCTGTTGTTGAAGTATCATCTGGTTTGCCTAACCTTAAATTGTA
 TATATTATCTGTTAGCTAATATTAAATTCAAATATCCCATATCTAAATTAGTGCAATAT
 CTTGTCTTGTATAGGTCAATGAATTCAAAATTATTATGTCTGTTATAGAATAAAGA
 TTAATATATGTTAAAAAAA

FIGURE 126

MGSGRRALSAVPAVLLVLTLPGLPVWAQNDTEPIVLEGKCLVVCDSPATDSKGSSSPLGI
SVRAANSKVAFSAVRSTNHEPSEMSNKTRIIYFDQILVNNGNFTTLESVFVAPRKGIYSFSF
HVIKVYQSQTIQVNMLNGKPVISAFAGDKDVTREAATNGVLLYLDKEDKVYLKLEKGNLVG
GWQYSTFSGFLVFPL

Signal peptide:

amino acids 1-27

FIGURE 127

CGGTGGCCATGACTGCGGCCGTGTTCTCGGCTGCGCCTCATTGCCTCGGGCCTGCGCTC
GCCCTTATGTCTTACCATGCCATCGAGCCGTTGCGTATCATCTTCCTCATGCCGGAGC
TTTCTTCTGGTTGGTGTCTACTGATTCGTCCCTGTTGGTCATGGCAAGAGTCATTA
TTGACAACAAAGATGGACCAACACAGAAAATATCTGCTGATCTTGGAGCGTTGTCTGTG
TATATCCAAGAAATGTTCCGATTTGCATATTATAAACTCTTAAAAAAAGCCAGTGAAGGTT
GAAGAGTATAAACCCAGGTGAGACAGCACCCCTATGCGACTGCTGGCTATGTTCTGGCT
TGGGCTTGGAAATCATGAGTGGAGTATTTCTTGTAATACCCATCTGACTCCTTGGGG
CCAGGCACAGTGGCATTCACTGGAGATTCTCCTCAATTCTCCTTATTCACTTCACTGAC
GCTGGTCATTATCTGCTGCATGTATTCTGGGCATTGTATTTTGATGGCTGTGAGAAGA
AAAAGTGGGCATCCTCCTATCGTTCTGACCCACCTGCTGGTGTCAAGCCCAGACCTTC
ATAAGTTCTTATTATGGAATAAACCTGGCGTCAGCATTATAATCCTGGTGTCACTGGCAC
CTGGGCATTCTTAGCTGCAGGAGGCAGCTGCCAAGCCTGAAACTCTGCCTGCTCTGCCAAG
ACAAGAACTTCTTACAACCAGCGCTCCAGATAAACCTCAGGAAACCAGCACTCCCAA
ACCGCAGACTACATTTAGAGGAAGCACAACGTGCCTTTCTGAAAATCCCTTTCTG
GTGGAATTGAGAAAGAAATAAAACTATGCAGATA

FIGURE 128

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658
><subunit 1 of 1, 257 aa, 1 stop
><MW: 28472, pI: 9.33, NX(S/T): 0
MTAAVFFGCAFIAFGPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDN
KDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGF
GIMSGVFSFVNTLSDSLGP GTVG I HGDSPQFFLYSAFMTLVIILLHVFWGIVFFDGCEKKW
GILLIVLLTHLLVSAQTFI SYYGINLASAFI I L VLMGTWAFLAAGGSCRS LKLCLLCQDKN
FLLYNQR SR
```

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domains:

amino acids 32-51, 119-138, 152-169, 216-235

Glycosaminoglycan attachment site.

amino acids 120-123

Sodium:neurotransmitter symporter family protein

amino acids 31-65

FIGURE 129

CGGCAACCAGCCGCCACCACCGCTGCCACTGCCGCCCTGCCGGGGCC**ATG**TTCGCTCTGGGCTTGCCCTTCT
 TGGTGCCTTGGTGGCCTCGGTGAGAGCCATCTGGGGTTCTGGGGCCAAGAACGTCTCGCAGAAAGACGCCG
 AGTTGAGCGCACCTACGTGGACGAGGTCACAGCGAGCTGGCAACATCTACACCTCAACCATACTGTGACCC
 GCAACAGGACAGAGGGCGTGCCTGAGCTGTGAACGTCCTGAACAAGCAGAAGGGGGCGCCGTTGCTGTTGTGG
 TCCGCCAGAAGGAGGCTGTGGTGCCTCCAGGTGCCCTAATCCTGCGAGGGATGTTCAGCGCAAGTACCTCT
 ACCAAAAAGTGGAACGAACCCGTGTCAGCCCCCACCAGAAGATGAGTCGGAGATTCAAGTCTTCTACGTGGATG
 TGTCACCCCTGTCACCAGTCACACACATACAGCTCCGGTCAGCGCATGGACGATTGTCAGGACTG
 GGGAGCAGTTCAGCTCAATACACAGCACAGCACAGCCCAGTACTTCAGTCAAGTATGAGTCCTGAAGGCCTGGACT
 CGGTAAATTGTCAGGTGACCTCAAAAGGCCCTCCCTGTCAGTCATCTCCATTAGGATGTGTCCTG
 TCTATGACCTGGAACAAACAGTAGCCTTCATCGCATGTACAGACGATGACCAAGAAGGGCCATACCGTAC
 AGCGAACAGACTTCCCAGCAACAGCTTTATGTTGTTGGTGAAGACCGAAGACCAAGCCTGCGGGGCT
 CCCTGCCTTCTACCCCTTCAGCAAGAGATGAACCGTCATCAAGGGCACCGCAGAAAACCTGTCAGTGCTGG
 TGTCTCAAGCAGTCACGTCAGGCACTACGTCAGTGGATGCTCTTTGCTGGTATATTCTCTCCTTAC
 TGCTGACCGTCTCCCTGGCTGCTGGAGAACGGAGAAGAAGAACCCCTGCTGGTGGCCATTGACCGAG
 CCTGCCAGAACAGGGTACCCCTGAGTCCTGGTGAATTCTTCCCTGGCAGTCCCTTATGAGGTTACA
 ATGGCTCCTTGAGAATGTTCTGGATCTACCGATGGTCTGGTGAACAGCGCTGGCACTGGGACCTCTCTTAC
 GTTACCAAGGGCGCTCCTTGAAACCTGTAGGTAACGGCCAGTGGACTCCATGAGCTCTGTGGAGGAGATG
 ACTACGACACATTGACCGACATCGATTCCGACAAGAATGTCATTGCAACAAAGCAATACCTCTATGTTGCTGACC
 TGGCACGGAAGGACAAGCGTGTCTGGGAAAAAGTACCAAGATCTACTTCTGGAACATTGCCACCATTGCTGTCT
 TCTATGCCCTCCTGTGGTGCAGCTGGTGAATGTCACAGGAATCAGGACATCT
 GCTACTACAACCTCCTCTCGGCCACCCACTGGCAATCTAGCGCCCTCAACACATCCTCAGCAACCTGGGG
 ACATCCTGCTGGGCTGCTTCTGCTCATCATCCTGCAACGGAGATCAACACACAGGGCCCTGCTGCCA
 ATGACCTCTGTGCCCTGGAATGTGGATCCCCAACACTTGGGTTCTACGCCATGGCACAGCCCTGATGA
 TGGAGGGCTGCTCAGTGTCTATCATGTGTGCCCAACTATACAAATTCCAGTGGACACATCGTCATGT
 ACATGATGCCGGACTCTGCATGTCAGCTAACAGCGGACCCGGACATCAACGCCAGCGCCTACAGTG
 CCTACGCCTGCCATTGTCATCTCTCTGCTGTGGCTGGTCTTGGCAAAGGGAACACGGCGTTCT
 GGATCGTCTCTCCATTCACATCGCACCTGCTCAGCACGCTCTATTACATGGCCGGTGG
 AACTGGACTCGGGGATCTTCGCCCATCTCCACGTGCTCTACACAGACTGCACTCCGGCAGTGCAGCGGGCCGC
 TCTACGTGGACCGCATGGTGTCTGGTACGGCAACGTCATCAACTGGTCGCTGGCTGCCATGGCTTATCA
 TGCGCCCAATGATTGCTCCTATTGTTGGCATTGGCATCTGCAACCTGCTCTTACTTCGCTTCTACA
 TCATCATGAAGCTCCGGAGGGAGAGGATCAAGCTCATCCCCCTGCTCTGCATGTTGCACCTCCGTGGTCT
 GGGCTCGGCTCTTCTTCTCAGGGACTCAGCACCTGGCAGAAAACCCCTGCAAGACTGAGGGAGCACA
 ACCGGGACTGCATCCTCTGACTTTGACGACCCACATCTGGCACTTCTCTCCATGCCATGTTCG
 GGTCTTCTGGTGTGTGCACACTGGATGACGACCTGGATACTGTGCAGCGGGACAAGATCTATGCTTCT**TAGC**
 AGGAGCTGGCCCTCGCTCACCTCAAGGGCCCTGAGCTCTTGTGTCATAGACCGGTACTCTGCTGCT
 GTGGGGATGAGTCCCAGCACCGCTGCCAGCAGTGGATGGCAGCAGGACAGCAGGTCTAGCTAGGCTTGGCCT
 GGGACAGCCATGGGGTGGCATGGAACCTGCACTGCCCTCTGCCAGGAGCAGGCCCTGCTCCCTGGAACCCCC
 AGATGTTGGCAAATTGCTGTTCTCAGTGTGGGCTTCCATGGGCCCTGCTCTTGGCTCTCCATT
 GTCCCTTGCAGAGAGGAGATGGAAGGGACACCCCTCCCCATTCTGCTGCCATTTGCCGCTCTCCCTCCCC
 ACAATGCCCAAGCCTGGGACCTAACGGCTCTTTCTCCCATACTCCACTCCAGGGCTAGTCTGGGGCTGA
 ATCTCTGCTGTATCAGGGCCCAAGTCTCTTGGGCTGCTCCCTGGCTGCCATCACTGCCCTTCCAGTCAGCC
 AGGATGGATGGGGTATGAGATTGGGGTGGCCAGCTGGTGCAGACTTGGTGTCAAGGCTGCAAGGGG
 CCTGGGGCAGTGCATCTCTCCCTGACCTGTGCTCAGGGCTGGCTCTTAGCAATGCGCTCAGCCAAATT
 TGAGAACCGCCTCTGATTCAAGAGGCTGAATTCAAGAGGCTCACCTTCAGGGCTCCATCCCACGCTCC
 AGCAGGACTGGAGGGAGAACGGCCCTACCCCTTCCCTCTTCCAGGGCCCTAGTCTTGCCTAACCCCC
 AGTCTGTGTTAGTCATGCACACACATACCTATGAAACCTTGGAGTTACAAAGAATTGCCCAAGCTCTGGG
 CCTGGCCACCCCTGGCTTGGATCCCCCTGCTCCACCTGGTCCACCCAGATGCTGAGGGATGGGGAGCTCAGG
 CGGGGCTCTGCTTGGGATGGGAATGTTCTCCAAACTGTTTATAGCTCTGCTGAAAGGGCTGG
 AGATGAGGTGGTCTGGATCTTTCTCAGAGCGTCTCCATGCTATGGTGCATTCCGTTCTATGAATGAATT
 TGCATTCAATAAACACAGACTCAAAAAAAAAAAAAA

FIGURE 130

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66659
><subunit 1 of 1, 832 aa, 1 stop
><MW: 94454, pI: 6.94, NX(S/T): 12
MFALGLPFLVLLVASVESHLGVLPKNVSQKDAEFERTYVDEVNSELVNITYTFNHTVTRNRT
EGVRVSVNVLNKQKGAPLLFVVRQKEAVVSFQVPLILRGMFQRKYLYQKVERTLCQPPTKNE
SEIQFFYVDVSTLSPVNNTYQLRVSRMDDFVLRTGEQFSFNTAAQPQYFKYEFPEGVDSVI
VKVTSNKAFPCSVISIQDVLCPVYDLDNNVAFIGMYQTMTKKAITVQRKDFPSNSFYVVVV
VKTEDQACGGSLPFYPFAEDEPVQDQGRQKTLSVLVSQAVTSEAYVSGMLFCLGIFLSFYLL
TVILLACWENWRQKKKTLVAIDRACPESGHPRVLADSFPGSSPYEGYNYSFENVSGSTDGL
VDSAGTGDLSYGYQGRSFEPVGTRPRVDSMSSVEDDYDTLDIDSDKNVIRTKQYLYVADL
ARKDKRVLRKKYQIYFWNIATIAVFYALPVVQLVITYQTVVNVTGNQDICYYNFLCAHPLGN
LSAFNNILSNLGYILLGLLFLLIILQREINHNRA LLRNDLCALECGIPKHGFLFYAMGTALM
MEGLLSACYHVCNPNTNFQFDTSFMYMIAGLCMLKLYQKRHPDINASAYSAYACLAIVIFFS
VLGVVFGKGNTAFWIVFSIIIIIATLLLSTQLYYMGRWKLD SGIFRRILHVLYTDCIRQCSG
PLYVDRMVLLVMGNVINWSLAAYGLIMRPNDFASYLLAIGICNLLYFAFYIIMKLRSGERI
KLIPLL CIVCTS VVWGFALFFFQGLSTWQKTPAESREHNRDCILLDFDDHDIWHFLSSIA
MFGSFLVLLTLDDDDTVQRDKIYVF
```

Important features of the protein:**Signal peptide:**

amino acids 1-18

Transmembrane domains:

amino acids 292-317, 451-470, 501-520, 607-627, 751-770

Leucine zipper pattern.

amino acids 497-518

N-glycosylation sites.

amino acids 27-30, 54-57, 60-63, 123-126, 141-144, 165-168, 364-367, 476-479, 496-499, 572-575, 603-606, 699-702

FIGURE 131

FIGURE 132

MVPAWLWLLCVSVPQALPKAQPAELSVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSG
KATEGPFAMDPDSGFLLVTRALDREEQAQEYQLQVTLEMQDGHVLWGPQPVLHVVKDENQVP
HFSQAIYRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQSPDMFQLEPRL
GALALSPKGSTS LDHALERTYQLLVQVKDMGDQASGHQATATVEVSIIESTWVSLEPIHLAE
NLKVLYPHHMAQVHWSGGDVHYHLESHPGPFEVNAEGNLYVTRELDREAQAEYLLQVRAQN
SHGEDYAAPLELHVLVMDENDNVPICPPRDPTVSIPELSPPGTEVTRLSAEDADAPGSPNSH
V VYQLLSPEPEDGVGRAFQVDPTSGSVTLGVPLRAGQNILLVLAMDIAGAEGGFSSTCE
VEVAVTDINDHAPEFITSQIGPISLPEDVEPGTLVAMLTAIDADLEPAFRLMDFAIERGDTE
GTFGLDWEPDGHVRLRLCKNLSYEAAAPSHEVVVVVQSVAKLVGPGPGATATVTVLVERV
MPPP KLDQESYEASVPISAPAGSFLLTIQPSDPISRTLRFSLVNDSEGWL CIEKFSGEVHTA
QSLQGAQPGDTYTVLVEAQDTALT LAPVPSQYLCTPRQDHGLIVSGPSKDPDLASGHGPYSF
TLGP NPTVQRDWRLQTLNGSHAYLT LALHWV EPREHIIIPVVVSHNAQM WQLLRVIVCRCNV
EGQCMRKVGRMKGMPTKLSAVGILVGT LVAIGIFLILIFT HWTMSRKKD P DQPADSVPLKATV

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 762-784

FIGURE 133

CCGGGGAC**ATG**GAGGTGGACTGTTCATTGGGGCCCTTATTGGGTCCAGCATCTGTGGCAA
 GAAAAAATTTTGGGGACCAAGTTGAGGATTAATGTCAGAAATGGAGACGAGATCAGCAA
 ATTGAGTCAACTAGTGAATTCAAACAACCTGAAGCTCAATTCTGAAATCTCCCTCCT
 TCAATCGGCCTGTGGATGTCCTGGTCCCCTGTCAAGTGCAGGCATTAAATCCTCCTG
 AGATCCCAGGGCTTAGAGTACGCAGTGACAATTGAGGACCTGCAGGCCCTTTAGACAATGA
 AGATGATGAAATGCAACACAATGAAGGGCAAGAACGGAGCAGTAATAACTCAACTACGGGG
 CTTACCATTCCCTGGAAGCTATTACACGAGATGGACAACATTGCCGCAGACTTCCTGAC
 CTGGCGAGGAGGGTGAAGATTGGACATTGTTGAAAACCGGCCATGTATGTAAGT
 CAGCACTGGAAAGGCGTGAGGGCGCCGGCGTTGGCTGAATGCAGGCATCCATTCCCGAG
 AGTGGATCTCCAGGCCACTGCAATCTGGACGGCAAGGAAGATTGTATGATTACCAAGGG
 GATCCAGCTATCACCTCCATCTGGAGAAAATGGATATTTCCTGTTGCCGTGGCCAATCC
 TGATGGATATGTGTATACTCAAACCTCAAACCGATTATGGAGGAAGACGCCGGTCCCGAAATC
 CTGGAAAGCTCCTGCATTGGTGCACCCAAATAGAAACTGGAACGCTAGTTGCAGGAAAG
 GGAGCCAGCGACAACCCCTGCTCCGAAGTGTACCATGGACCCCACGCCAATTGGAAGTGG
 GGTGAAATCAGTGGTAGATTTCATCCAAAACATGGGAATTCAAGGGCTCATCGACCTGC
 ACAGCTACTCGCAGCTGCTGATGTATCCATATGGGTACTCAGTCAAAAGGCCAGATGCC
 GAGGAACCTCGACAAGGTGGCGAGGCTTGCAGGCCAAAGCTCTGGCTCTGTGTCGGGACTG
 GTACCAAGTGGTCCACCTGCACCACTGTCTATCCAGCTAGCGGGAGCAGCATGACTGG
 CGTATGACAACGGCATCAAATTGCAATTGAGTTGAGAGATACCGGGACCTATGGC
 TTCCTCCTGCCAGCTAACAGATCATCCCCACTGCAGAGGAGACGTGGCTGGGCTGAAGAC
 CATCATGGAGCATGTGCGGGACAACCTCTAC**TAG**GCGATGGCTGCTCTGTCTACATT
 TTGTACCCACACGTGCACGCACTGAGGCCATTGTTAAAGGAGCTTCCACCTGTGAG
 TCAGAGCCCTCTGGGTTGTGGAGCACACAGGCCCTGCCAGCCAGCTCCGGAGT
 CGTGTGTCCTGGCGGTGTCCTGCAAGAACACTGGTCTGCCAGCCTGCTCAATTGGCCTG
 CTGTTTTGATGAGCCTTGTCTGTTCTCCACCTGCTGGCTGGCGCTGCACTC
 AGCATCACCCCTCCTGGTGGCATGTCCTCTACCTCATTAGAACAAAGAACATC
 TGAGATGATTCTCTACCCATCCACATCTAGCCAAGCCAGTGCACCTGCTCTGGGGACT
 GTGGGAGACACCACCTGTCTTAGGTGGGTCTCAAAGATGATGTAGAATTCCCTTAATT
 TCGCAGTCTCCTGGAAAATATTCCCTTGAGCAGCAAATCTGTAGGGATATCAGTGAAG
 GTCTCCCTCCCTCTGTTTTTTGAGACAGAGTTGCTCTGTG
 CAGGCTGGAGTGTGATGGCTCGATCTGGCTACCACACCTCTGCCCTGGGTTCAAGCA
 ATTCTCCTGCCCTGCGCTTGTGAGTAGCTGGTTATAGGCGCATGCCACCATGCCCTGGCTA
 ATTTTGTGTTTTAGTAGAGACAGGGTTCTCCATGTTGGTCAGGCTGGCTCAAACCTCCCA
 ACCTCAGGTGATCTGCCCTCTGGCCTCCAGAGTGTGGATTACAGGTGTGAGCCACTG
 TGCCGGGCCGTCCTCTGGGCTTGTGAGAACAAAGTAGAAGATCAGTGTG
 TGTGCTGAGAATTCTAGATACTACAGTCTACTCCTCTTGTGTTATTCAAGTGTG
 ACCAGGATGGCGGGAGGGATCTGTGTCAGTGTAGGTACTGTGCCAGGAAGGCTGGGTGAA
 GTGACCACATCAAATTGCAAGGATGGTGAATTATCCCCATCTGCTTAATGGGCTTACCTCCT
 CTTGCCTTGTGAACTCACTCAAAGATCTAGGCCTCATCTTACAGGTCTAAATCACTCAT
 CTGGCCTGGATAATCTCACTGCCCTGGCACATTCCATTGTGCTGTGTTGTTGTTGTT
 TCCTTGTGCTGGTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT
 TCTGTCTATTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT
 GCCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT
 TTGTTTTTGCTTACCAAACATGTGTAATCTAACCTCCTGCCAGGATTGTACA
 GCATCTGGTGTGCTTATAAGCCAATAATATTCAATGTGAAAAAAAAAAAAAA

FIGURE 134

MRWILFIGALIGSSICGQEKKFFGDQVLRINVRNGDEISKLSQLVSNNLKLNFWKSPSSFNR
PVDVLVPSVSLQAFKSFLRSQGLEYAVTIEDLQALLDNEDDEMHQNEGQERSNNFNYGAYH
SLEAIYHEMDNIAADFPDLARRVKIGHSFENRPMYVLKFSTGKVRRPAVWLNAGIHSREWI
SQATAIW TARKIVSDYQRDPAITSILEKMDIFLLPVANPDGYVYTQTQNRLWRKTRS RNP G S
SCIGADPNRNWNASFAGKGASDNPCSEVYHGPHANSEVEVKS VVDFIQKHGNFKGFIDLHSY
SQLLMYPYGYSVKKAPDAEELDKVARLAAKALASVSGTEYQVGPTCTTVYPASGSSIDWAYD
NGIKFAFTFELRDTGTGYGFLIPANQI IPTAEETWLGLKTIMEHVRDNLY

Signal peptide:

amino acids 1-16

FIGURE 135

FIGURE 136

MASYLYGVLFAGVLCAPIVCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLE
TPSQNIFFSPSVSTSLAMLSLGAHSVTKTQILQGLGFNLHTPESAIHQGFQHLVHSLTVP
SKDLTLKMGSALFVKKELOLQANFLGNVKRLYEAEVFSTDPSNPSIAQARINSHVKKKTQGK
VVVDIIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQVTVQVPMMHQKEQFAF
GVDTELNCFVLQMDYKGDAVAFFVLPSPKGKMRQLEQALSARTLIKWSHSLQKRWIEVFIPRF
SISASYNLETILPKMGIQNAFDKNADFGIAKRDSSLQVSKATHKAVLDVSEEGTEATAATT
KFIVRSKDGPSYFTVSFNRTFLMMITNKATDGILFLGKVENPTKS

Signal peptide:

amino acids 1-20

FIGURE 137

GGCTGACCGTGCTACATTGCCTGGAGGAAGCCTAACCGAACCAGGCATCCAGCTGCCACGC
 CTGAGTCCAAGATTCTCCCAGGAACACAAACGTAGGAGACCCACGCTCCTGGAAGCACCAG
 CCTTTATCTCTCACCTCAAGTCCCCTTCTCAAGAACATCCTCTGTTCTTGCCTCTAAAG
 TCTTGGTACATCTAGGACCCAGGCATCTTGCTTCCAGGCCACAAAGAGACAG**ATGAAGATGC**
 AGAAAGGAAATGTTCTCTTATGTTGGTCTACTATTGCATTAGAAGCTGCAACAAATTCC
 AATGAGACTAGCACCTCTGCCAACACTGGATCCAGTGTGATCTCAGTGGAGCCAGCACAGC
 CACCAACTCTGGGTCAGTGTGACCTCCAGTGGGTCAAGCACAGCCACCATCTCAGGGTCCA
 GCGTGCACCTCCAATGGGTCAGCATAGTCACCAACTCTGAGTTCCATACAACCTCCAGTGGG
 ATCAGCACAGCCACCAACTCTGAGTTCAGCACAGCGTCAGTGGGATCAGCATAGGCCACCAA
 CTCTGAGTCCAGCACAACCTCCAGTGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAC
 CCTCCAGTGGGCCAGCACAGTCACCAACTCTGGTCCAGTGTGACCTCCAGTGGAGCCAGC
 ACTGCCACCAACTCTGAGTCCAGCACAGTCAGTGTCCAGTAGGGCCAGCACTGCCACCAACTCTGA
 GTCTAGCACACTCTCAGTGGGCCAGCACAGCCACCAACTCTGACTCCAGCACAACCTCCA
 GTGGGCTAGCACAGCCACCAACTCTGAGTCCAGCACACCTCCAGTGGGCCAGCACAGCC
 ACCAACTCTGAGTCCAGCACAGTCAGTGTCCAGTAGGGCCAGCACTGCCACCAACTCTGAGTCCAG
 CACAACCTCCAGTGGGCCAGCACAGCCACCAACTCTGAGTCCAGAACGACCTCCAATGGG
 CTGGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGCCAGCACAGCCACCAAC
 TCTGACTCCAGCACAGTCAGTGTCCAGTGGGCCAGCACTGCCACCAACTCTGAGTCCAGCACGAC
 CTCCAGTGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGCTAGCA
 CAGCCACCAACTCTGACTCCAGCACAACTCCAGTGGGCCAGCACAGCCACCAACTCTGAG
 TCCAGCACAGTCAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACACCCCTCCAG
 TGGGCCAACACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGGGCCAACACAGCCA
 CCAACTCTGAGTCCAGCACAGTCAGTGTCCAGTGGGCCAGCACTGCCACCAACTCTGAGTCCAGC
 ACAACCTCCAGTGGGTCAAGCACAGCCACCAACTCTGAGTCCAGCACAAACCTCCAGTGGG
 TAGCACAGCCACCAACTCTGACTCCAGCACAAACCTCCAGTGGGCCAGCACAGCCACCAACT
 CTGAGTCTAGCACAGTCAGTGTGGATCAGCACAGTCACCAATTCTGAGTCCAGCACAAACC
 TCCAGTGGGCCAACACAGCCACCAACTCTGGTCCAGTGTGACCTCTGAGGCTCTGGAAC
 AGCAGCTCTGACTGGAATGCACACAACCTCCCATAGTCATCTACTGCAGTGAGTGAGGCAA
 AGCCTGGTGGTCCCTGGTGCCTGGAAATCTCCTCATCACCCCTGGTCTCGGTGTGGCG
 GCCGTGGGCTCTTGCTGGCTCTTCTGTGAGAAACAGCCTGTCCTGAGAAACAC
 CTTAACACAGCTGTCTACCACCCATGGCTCAACCATGGCTTGTTCCAGGCCCTGGAG
 GGAATCATGGAGCCCCCACAGGCCAGGTGGACTCTAACCTGGTCTGGAGGAGACCAGTA
 TCATCGATAGCCATGGAGATGAGCAGGGAGGAACAGCAGGCC**TGA**GCAGCCCCGGAAAGCAAG
 TGCCGCATTCTCAGGAAGGAAGAGACCTGGCACCCAAAGACCTGGTTCTTCTTCAATTCTCACC
 CCAGGAGACCCCTCCAGCTTGTGAGATCCTGAAAATCTGAGAAGGTATTCTCATTCTCACC
 TTTCTGCCTTACCAAGACACTGGAAAGAGAAATACTATATTGCTCATTAGCTAAGAAATAA
 ATACATCTCATCTAACACACACGACAAAGAGAAAGCTGTGCTTGCCTGGACTCCATCTGGCATTCAAAA
 CTCTGAGATGAACACTAGTTAGGAGAAAACCTCCATGCTGGACTCCATCTGGCATTCAAAA
 TCTCCACAGTAAATCCAAAGACCTCAAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAA

FIGURE 138

MKM**Q**GNVLLMFGLLHLEAATNSNETSTSANTGSSVISSGASTATNGSSVTSSGVSTATI
SGSSVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSE
SSTPSSGASTVTNGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSS
TTSSGASTATNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTT
SNGAGTATNSESSTTSSGASTATNDSSTVSSGASTATNSESSTTSSGASTATNSESSTTSS
GASTATNDSSTTSSGAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGA
NTATNSESSTVSSGASTATNSESSTTSSGVSTATNSESSTTSSGASTATNDSSTTSEAST
ATNSESSTVSSGISTVTNSESSTTSSGANTATNGSSVTSAGSGTAALTGMHTTSHSASTAV
SEAKPGGSLVPWEIFLITLVSVVAAVGLFAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGP
GPGGNHGAPHRPRWSPNWFWRPVSSIAMEMSGRNSGP

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 510-532

FIGURE 139

GGGAGAGAGGATAAATAGCAGCGTGGCTTCCCTGGCTCCTCTGCATCCTCCGACCTTC
CCAGCAATATGCATCTTGCACGTCTGGTCGGCTCCTGCTCCCTCCTCTGCTACTGGGGCC
CTGTCTGGATGGCGGCCAGCGATGACCCCATTGAGAAGGTATTGAAGGGATCAACCGAGG
GCTGAGCAATGCAGAGAGAGAGGTGGCAAGGCCCTGGATGGCATCAACAGTCCAATCACGC
ATGCCGGAAGGGAAAGTGGAGAAGGTTCAACGGACTTAGCAACATGGGAGCCACACCGGC
AAGGAGTTGGACAAAGCGTCCAGGGCTAACCAACGGCATGGACAAGGTTGCCATGAGAT
CAACCATGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGTCAACAAACG
CTGCTGGACAGGCCGGAAAGGAAGCAGACAAAGCGGTCCAAGGGTTCCACACTGGGTCCAC
CAGGCTGGGAAGGAAGCAGAGAAACTTGGCCAAGGGTCAACCATGCTGCTGACCAGGCTGG
AAAGGAAGTGGAGAAGCTTGGCCAAGGTGCCACCATGCTGCTGGCCAGGCCGGAAAGGAGC
TGCAGAATGCTCATAATGGGTCAACCAAGCCAGCAAGGGAGGCCACAGCTGCTGAATGGC
AACCATCAAAGCGGATCTCCAGCCATCAAGGAGGGCCACAACCACGCCGTTAGCCTCTGG
GGCCTCAGTCAACACGCCATTCAACCTTCCGCCGTGGAGGAGCGTCGCCAACATCA
TGCCCTAAACTGGCATCCGGCTTGCTGGAGAATAATGTCGCCGTTGTACATCAGCTGAC
ATGACCTGGAGGGTTGGGGGACAGGTTCTGAAATCCCTGAAGGGGGTTGTACTG
GGATTGTGAATAACTTGATACACCA

FIGURE 140

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675
><subunit 1 of 1, 247 aa, 1 stop
><MW: 25335, pI: 7.00, NX(S/T): 0
MHLARLVGSCSLLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAG
REVEKVFNGLSNMGSHTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHGVNNAAG
QAGKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQN
AHNGVNQASKEANQLLNGNHQSGSSSHQGGATTPLASGVNTPFINLPALWRSVANIMP
```

Important features of the protein:

Signal peptide:

amino acids 1-25

Homologous region to circumsporozoite (CS) repeats:

amino acids 35-225

FIGURE 141

CTCCGGGTCCCCAGGGGCTGCGCCGGCGGCTGGCAAGGGGGACGAGTCAGTGGACACTCCAGGAAGAGCGGC
 CCCCGGGGGCGATGACCGTGCCTGACCTGACTCACTCCAGGTCGGAGGGGGCCCCGGGGCAGTC
 GGGCGGACCGCGGGCGAGCTGCCGCCGTGAGTCGGGCCAGCCACCTGAGCCCAGGCCGGGACACCGTC
 GCTCCTGCTCTCGA**ATG**CTGCGACCGCGATGGGCCTGAGGAGCTGGCTGCCGCCCATGGGCCTGCC
 CCTCGGCCACCGCTGCTGCTCTGCTGCTGCTGCTGAGCCGCCATTCTCAGATTGAAGCTGAACACATCTCA
 CCCGGATCAGCCTGCCTGGGCTCTGAAGAGCGGCCATTCTCAGATTGAAGCTGAACACATCTCA
 ACAGCCCTCTGCTGAGCAGGGATGCCAGGACCTGTAACGGGTGCTCGAGAGGCCCTCTTGCACTCAGTAGC
 AACCTCAGCTTCTGCCAGGGAGTACCAAGGAGCTGCTTGGGTGAGACGAGAGAAACAGCAGTC
 AGCTTCAAGGGCAAGGACCCACAGCGCAGTCAGGAAACATCAAGATCCTCTGCCGCTCAGCAGTC
 CTGGTCACCTGTGGCACAGCAGCCTCAGCCCCATGTGTAACCTACATCAACATGGAGAACCTCACCC
 GAGGAAAGGGAAATGTCCTCTGGAGATGCCAGGGCCGGTTGTCCTTCAGCCGAATTCAAGTCCACTGCC
 CTGGTGGTTGATGGCGAGCTCTACACTGGAACAGTCAGCAGCTCCAAGGGAATGACCCGCCATCTCGGGAGC
 CAAAGCCTTCGCCCCACCAAGACCGAGAGCTCCCTCAACTGGCTGCAAGACCCAGCTTTGTCGGCTCAGC
 ATTCTGAGAGCCTGGCAGCTTGCAGGCCAGTGTGACAAGATCTACTTTTCTCAGCGAGACTGCCAGGAA
 TTTGAGTTCTTGAGAACACCATTGTGTCGGCATTGCCGCATCTGCAAGGGCAGTGAAGGGTGGAGAGCGGGTG
 CTACAGCAGCGCTGGACCTCTCAAGGCCAGCTGCTGTCAGGCCAGATGGCTTCCCTCAAC
 GTGCTGAGGATGTCTCACGCTGAGCCCAGGCCAGGACTGGCGTGACACCTTTCTATGGGTCTTC
 TCCCAGTGGCACAGGGAAACTACAGAAGGCTGCGCTGTGTCACAATGAAGGATGTGAGAGAGTC
 AGCGGCCTCTACAAGGAGGTGAACCGTGAGACACAGCAGTGGTACACCGTGACCCACCCGGTGC
 CCTGGAGCGTGCATCACCAACAGTGCCGGAAAGGAAGATCAACTCATCCCTGCACTCCAGGCCGTGCTG
 AACCTCTCAAGGACCACTCTCTGATGGACGGCAGGTCCGAAGGCCAGTGTGCTGCTGCCAGGCCAGGCTCG
 TACCAAGCGCGTGGCTGTACACCGCGTCCCTGGCTGCACACACCTACGATGTCCTCTTCCTGGCAGTGGTGAC
 GGCCGGCTCCACAAGGCAGTGAGCGTGGGCCGGGGTGACATCATTGAGGGAGCTGCAAGATCTTCTCATCG
 CAGCCCCGTGCAAACTGCTCTGACACCCACAGGGGGCTGCTGTATGCCCTCACACTCGGGCTAGTCCAG
 GTGCCCATGGCAACTGCAAGCCTGTACCGGGAGCTGTGGGACTGCCCTCGCCGGGACCCCTACTGTGCTTG
 AGCGGCTCCAGCTGCAAGCAGCTGACGCTCACCGCTCAGCTGGCCACCAGGCCGTGGATCCAGGACATCG
 GGAGGCCAGGCCAAGGGACCTTGCGCGTCTCGGTTGTGTCCTCGTCTTGTACCAACAGGGAGAACGCA
 TGTGAGCAAGTCCAGTTCAAGCCAAACACAGTGAACACTTTGGCCTGCCGCTCTCCTCAACCTGGCAGCC
 CTCTGGCTACGCAACGGGCCCCCGTCAATGCCCTGCCACGTGCTACCCACTGGGACCTGCTGCTG
 GTGGGCACCCAACAGCTGGGGAGTTCCAGTGCTGGTCACTAGAGGGGCTTCCAGCAGCTGGTAGCCAGCTAC
 TGCCAGAGGTGGAGGACGGGTGGCAGACCAAACAGATGAGGGTGGCAGTGTACCGTCAATTACAGCACA
 TCGCGTGTGAGTGCACCAAGCTGGGGCAAGGCCAGCTGGGTGCAAGACAGGTCTACTGGAAGGAGTCTGGT
 ATGTGACGCTCTTGCTGGCGTGTGCTCCCAGTTTATTCTGCTCTACCGCACCGAACAGCATGAAA
 GTCTCTGAAGCAGGGGAATGTGCCAGCGTGCACCCCAAGACCTGCCCTGTGGTGTGCCCTGAGACCC
 CCACTCAACGGCTAGGGCCCCCTAGCACCCGCTCGATCACCAGGGTACAGTCCCTGTCAGACAGCCCC
 GGGGCCGAGTCTCACTGAGTCAGAGAACAGGCCACTCAGCATCCAAGACAGCTCGTGAGGTATCCCAGTG
 TGCCCCCGGCCCCGGTCCGCCCTGGCTGGAGATCCGTACTCTGGTG**TGA**GAGCTGACTTCAAGAGGACGC
 TGCCCTGGCTCAGGGCGTGTGAATGCTCGGAGAGGGTCAACTGGACCTCCCGCTCGCTCTCGTGGAAAC
 ACGACCGTGGTGGCGGCCCTGGAGGCCCTGGAGCCAGCTGGCTGCTCTCCAGTCAAGTAGCGAAGCTCC
 TACCAACCCAGACACCCAAACAGCGTGGGCCAGAGGTCTGGCAAATATGGGGCTGCCCTAGGTGGTGGAA
 CAGTGCTCCTATGTAACAGGCCCTTGTAAAAAAACAATTCCAATGTAACAGGAAACTAGAAATGAGAGGGAAAGAG
 ATAGCATGGCATGCAGCACACACGGCTGCTCAGTTGATGCCCTCCAGGGGTGCTGGGGATGCATCAAAGTGG
 TTGTCAGACAGAGTTGGAAACCCCTACCAACTGCCCTTCCACCTTCCACATTACCGCTGCCACCGGCTGC
 CCTGTCACTGCAGATTCAGGACAGCTGGCTGCGTTCTGCTGCCAGTCAAGCCAGGATGTAGTTG
 TTGCTGCCGTGTCCTGGACCTTCCAGGCCCTGATCAGGCTGTTGCACTGCCCTCAGGCTCTGGC
 GGACCCAACCTCTGGACCTTCCAGGCCCTGATCAGGCTGTTGCACTGCCCTCAGGCTCTGGC
 TTTCGTACAATGTACGCCCTTCCCTCAGAAATTCAAGGGAGAGACTGTCGCCCTGCCCTCCGTTGCGTGA
 GAACCGGTGTGCCCTTCCCACCATATCCACCCCTCGCTCATCTTGAACCAAACACGAGGAACACTA
 ACTGCACCTGGTCTCCCCAGTCACCCCTCACCTCCACTCTAAGGGATATCAACACTGCC
 AGCACAGGGGCCCTGAATTATGTTGGTTTATACATTAAATAAGATGCACTTATGTCATTAAATAAAA
 GTCTGAAGAATTACTGTTAAAAAAAAAAA

FIGURE 142

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962
><subunit 1 of 1, 837 aa, 1 stop
><MW: 92750, pI: 7.04, NX(S/T): 6
MLRTAMGLRSWLAAPWGALPPRPLL LLLLQPPPPTWALSPRISLPLGSEERPFLRF
EAEHISNYTALLLSRDGR TL YVGAREALFALSSNLSFLPGGEYQELLWGADAEEKKQQCSFKG
KDPQRDCQNYIKILLPLSGSHLFTCGTAAFSPMCTYINMENFTLARDEKG NVLLEDGKGRC P
FD PNFKSTALVVDGE LY TGT VSS FQGNDPAISRSQSLRPTKT ESSLNWLQDPAFVASAYIPE
SLGSLQGDDD KIYFFFSETGQEFEFFENTIVSRIARI CKGDEGGERVLQQRWTSFLKAQLLC
SRPDDGF PNVLQDVFTLSPSPQDW RDTLFYGVFTSQWHRGTTEGSACVFTMKDVQRVFSG
LYKEVNRETQQWYT VTHPVPTPRPGACITNSARERKINSSLQLPDRVLNFLKDHFLMDGQVR
SRM LLLQPOQARYQRVAVHRVPGLHHTYDVLFLGTGDGR LHKA VSVGPRVHIIIEELQIFSSGQ
PVQNLLLDTHR GLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSGSSCKHVSLYQP
QLATRPWIQDIEGASAKDLC SASSVVSPSFVPTGEKPCEQVQFQPN TVNTIACPLLSNLATR
LWL RNGAPVN ASASCHVLPTGD LLLVGTQQLGEFQCWSLEEGFQQLVASYCPEVVEDGVADQ
TDEGGSVPII I STSRV SAPAGG KASWGADRSY WKEFLVMCTLFVLA VLLPVL FLLYRHRNSM
KVFLKQGECASVHPK TCPVVLPPETRPLNGLGPPSTPLDHRGYQSLSDSPPGARVFT ESEKR
PLSIQDSFVEVSPVCPRPRVRLGSEIRDSVV
```

Transmembrane domains:

amino acids 23-46 (type II), 718-738

FIGURE 143A

CTAAGCCGGAGGATGTGCAGCTGCCGGCGCCGGCTACGAAGAGGACGGGGACAGGCCGGTGCAGACCGA
GCCCAAGCCAGCCGGAGGACGCCGGCAGGGCAGGGAGCCCCGACTCGTCTGCCGCCGCGCTCGCCGCTCG
TGCCGGCCCCCGCTCCCCGCCGCGAGCGGGAGGAGCCGCCACCTCGGCCGAGCCGCCGCTAGCGCGC
CGGGCATGGTCCCCCTTAAAGGCGCAGGCCGCCGGCGGGGGGGTGTGCGGAACAAAGGCCGGCGGGGG
CCTGCGGCGGCTCGGGGCCGATGGCGCAGGCCGCCGGCGCGCGCTGCCCGGCCGGCGCTCG
CGCGCTAGGGCGGGCTGGCTCCGTGGCGGGGGCAGCGGGCTGAGGGCGCGAGCCTGCCGGCG
GGCGCGGCCGCCGGCGGGCGAGCGCGCGGGCAGTCGCGCAGGCCCTGCCGCTAGCGTGC
TGCTCGGGCTCGTCTGGCTCGTCTGCCGCCGCTCGTCTGCCCGGCCGCCGCTTCCAGCTGAAGCGAGCG
GCCCACGGCGCCGCCAGCCCCGAGGGCTGCCGGTCCGGGAGGCCGCCGGCTCCAGGCCGCCGGCGCG
GCGATGCCGCCGGCGCAGCTCTGGCCGCCGGCTCGGACCCAGATGGCGGCCGCCGCGACAGGAACCTTCCT
TCGTGGGAGTCATGACCGCCAGAAATACCTGCAGACTCGGGCGTGGCCGCCCTACAGAACATGGTCCAAGAACAA
TTCCCTGGGAAAGTTCAGTTCTCTCAAGTGAGGGTCTGACACATCTGACCAATTCCAGTAGTGCACACTACGG
GTGTGGGAGACTCTTACCCGGCCCAGAAGAACATGCTCATGATGCTCAAGTACATGCCAGGACCAACTTGGACA
AGTATGAATGGTTATGAGAGCAGATGACGTGATCACAAAGGAGACCGTCTGGAGAACCTTCTGAGGAGTT
TGAACAGCAGCGAGCCCCCTTCTTCTGGCAGACAGGCCCTGGCACCACGGAAGAACATGGGAAACTGCCCTGG
AGCCTGGTGAGAACCTCTGCATGGGGGCCCTGGCGTGTATGAGCCGGAGGTGCTTCCGGAGAACATGGTGCC
ACATTGGCAAGTGTCTCCGGAGATGTACACCACCATGAGGACGTGGAGGTGGGAAGGTGTGTCGGAGGTTG
CAGGGGTGAGTGTCTGGCTTATGAGATGCCAGCTTTTATGAGAACATGAGCAGAACAAAAGGGG
ACATTAGAGATCTCCATAACAGTAAATTCAACAGCTATCACATTACACCCCAACAAAAACCCACCCCTACCAAGT
ACAGGCTCCACAGCTACATGCTGAGCCGAAGATATCCGAGCTCCGCCATGCCACAATACAGCTGACCGC
TTGTCTGTAGAGCAAATACAGCAACACAGAAATTCAAAAGAGGACCTCAGCTGGGAATCCCTCCCTCCTCA
TGAGGTTTCAAGCCCCGCCAGCGAGAGGAGATTCTGGAATGGGAGTTCTGACTGGAAAATACTTGTATTGCCAG
TTGACGCCAGCCCCCTGAAAGAGGAATGGACTCCGCCAGAGGGAAGCCTTGGACGACATTGTCTGAGGTCA
TGGAGATGATCAATGCCAACGCAAGACCAGAGGGCGCATATTGACTTCAAAGAGATCCAGTACGGCTACCGC
GGGTGAACCCCATGTATGGGCTGAGTACATCTGGACCTGCTGCTCTGTACAAAAGCACAAAGGAAGAAA
TGACGGTCCCTGTGAGGAGGCACCGTATTACAGCAGACTTCAGCAAATCCAGTTGTGGAGCATGAGGAGC
TGGATGACAAGAGTTGCCAAGAGAACATCAATCAGGAATCTGGATCCTTGTCTTCTCTCAAACCTCCCTGAAGA
AGCTCGTCCCTTCAAGCTCCCTGGTCAAGAGTGTGAGCACAAAGAACCCAAAGATAAAAAGATAAACATACTGA
TCCCTTGTCTGGCGTTGACATGTTGTGAGATTATGGGAAACTTGTGAGAACAGCTGTCTTATCCCCAATC
AGAACGCTCAAGCTGTGGTCTGCTTCAATTCTGACTCCAACCCCTGACAAGGCCAACAAAGTGAACGTGATGA
GAGATTACCGCATTAAAGTACCTAAAGGCCACATGCAAGATTTCAGCTGTGCTGGAGAGTTTCAAGGCCCTGG
CCCTGGAAAGTAGGATCCTCCAGTTAACATGAATTTCAGCTTCTGCTCTGCCAGCTGTGCTTACT
CAGAACATTCTCAGCGATGTCGAGCACAAATCAGTTCTGGCCAACAAATATATTCCAATCATCTCAGGCC
ATGACCCAAAGATTGTTATAGTGGAAAGTTCCAGTGACAAACCATTTGCCCTTACTCAGAAAATGGCTTCT
GGAGAAACTATGGTTTGGCATACGTGATTATAAGGGAGATCTGTGCGAGTGGGTGGCTTGTGATGTTCCA
TCCAAGGCTGGGGCTGGAGGATGTGGACCTTTCAACAAGGTTGTCAGGCCAGGTTGAAGACGTTAGGAGC
AGGAAGTAGGAGTAGTCCACGTCACCATCTGTCTTGTGATCCAATCTGACCCAAACAGTACAAAATGT
GCTGGGGTCCAAAGCATGACCTATGGGCCACCCAGCAGCTGGCTGAGATGTGGCTGGAAAAAAATGATCCA
GTTACAGTAAAGCAGCAATAATGGCTCAGTGAGGACAGCTAAATGTCAGCTTGTGAGGAGACGCTTGTG
TAATTATCTAATTATTTTCAAAAATTGGTATGATCAGTTTGTGAGTCCGATACAAGGATATATTTCAC
AAAGTGGTTTCTTACATAGGACTCTTTAAGATTGAGCTTCTGAAACAAGAGGTGATCAGTGTGTTGCC
CACATCTCTGCTGAACATTATGAGCAGACCTGCTTAACCTGACTGAAATGTACCTGATGAACAAAACCTT
TTTAAAAAAATGTTCTTGTGAGACCCCTTGCTCAGTCCTATGGCAGAAAACGTGAACATTCTGCC
TATTGTAACAAAACACTGTAACCTCTGGTAAATGTTGTGATTGTTAACATTCCACAGATTCTAC
GTTTGTTTGTGTTTACATTGTTAAAGCCATTCTGCTTCAAGGTTGTAAGAACAGGAAATGTGATAATA
GCTGTTCTGCTTACATTGCTCAGGAGAGCTTCCAGAGTGTGATCATTCTCTCATGGTACTCTGCTCG
CACCGTAGGTTTGTGTTCTGCTTCAAGGAGAGCTCAGTCACCTGTTACCCAGGCTGGAAATG
CAGTGGCGCAACTCTGGCTCATTAACTCCACCTCCGGTCAAGCAATTCCCTGCCCTGGCTCC
AGCTGGGATTACAGGCACACACCACGCCAGNTAGTTTGTGATTGTTAGTAGAGACGGGTTTACCAT
GCAAGGCCAGCTGGCCACGTAGGTTAAAGCAAGGGCGTGAAGAAGGCACAGTGAGGATGTGGCTG
TGGTAGTTCTGCTCAGAGCTGCCATTCTGAGTACCTGTTAGTTAGTATTATGTTG
CTCTTTAAAGGGTAAATATTAAAGTGGTAACTGACAAAGATGAAATTACAAATACTGATG
GAAACATACACACATACACCCCTAATCAAAACGTTGGGGAAAATGTATTGGTTTGT
TGTTATGTTGAGATGGTTTCAATTCTTCAACTGTTGTTTATCCTTGATCTGAA
TTTATTAAATCTGTTGAGAGCTGCCATTCTGAGTACCTGTTAGTTAGTATTATGTTG
GAGTGTGTTAGTCTGTTTATTGAGTAAACCGATCTCCAAAGATTCCTTGG
GAGCTTCTGTTCC

FIGURE 143B

TTAATTTATATTCTTACTGTTTACTAAATATTAAGTGTTCTTGACAATTTGGTGCTCATGTGTTGGG
GACAAAAGTGAATGAATCTGTCATTATACCAGAAAGTTAAATTCTCAGATCAAATGTGCCTTAATAAATTGTT
TTCATTTAGATTCAAACAGTGATAGACTTGCCATTAAATACACGTCATTGGAGGGCTCGTATTGTAAATAG
CCTGATGCTCATTGGAAAAATAAACCAAGTGAACAATATTTCTATTGTACTTTCGAACCATTTGTCTCATT
ATTCCCTGTTTAGCTGAAGAATTGTATTACATTGGAGAGTAAAAACTAAACACGAAAAAA

FIGURE 144

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836
><subunit 1 of 1, 802 aa, 1 stop
><MW: 91812, pI: 9.52, NX(S/T): 3
MAARGRRRAWLSVLLGLVLGFVLASRLVLPRASELKAGPRRRASPEGCRSGQAAASQAGGAR
GDARGAQLWPPGSDDPGGPRDRNFLFVGVMTAQKYLQTRAVAAYRTWSKTIPGKVQFFSSEG
SDTSVPPIPVLGVDDSYPPQKSFMMALKYMDHYLDKYEFMRADDDVYIKGDRLENFLR
SLNSSEPLFLGQTGLGTTEEMGKLALEPGENFCMGGPGVIMSREVLRRMVPHIGKCLREMYT
THEDVEVGRCVRRFAGVQCVWSYEMRQLFYENYEQNKKGYIRDHLHSKIHQAITLEHPNKNPP
YQYRLHSYMLSRKISELRHRTIQLHREIVLMSKYSNTEIHKEDEIQLGIPPSFMRFQPRQREE
ILEWEFLTGKYLYSAVDGQPPIRGMDSAQREALDDIVMQVMEMINANAKTRGRIIDFKEIQY
GYRRVNPMYGAEYILDLLLLYKKHKGKMTVPVRRHAYLQQTFSKIQFVEHEELDAQELAKR
INQESGSLSLFLNSLKKLVPFQLPGSKSEHKEPKDKKINILIPLSGRFDMFVRFMGNFEKTC
LIPNQNVKLVVLNFNSDSNPDKAKQVELMRDYRIKYPKADMQILPVSGEFSRALALEVGSSQ
FNNESSLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQYDPKIVYSGKVPSDNHFAFT
QKTGFWRNYGFGITCIYKGDLVRVGGFDVSIQGWGLEDVDFNKVVQAGLKTFRSQEVGVVH
VHHPVFCDPNLDPKQYKMCLGSKASTYGSTQQLAEMWLEKNDPSYSKSSNNNGSVRTA
```

Signal peptide:

amino acids 1-23

FIGURE 145

GGACAACC GTT GCTGGGTGTCCCAGGGCCTGAGGCAGGCAGGTACTCCGCTGACACCTTCCC
 TTTCGGCCTTGAGGTTCCCAGCCTGGTGGCCCCAGGACGTTCCGGTCGCATGGCAGAGTGCT
 ACGGACGACGCTGAAGCCCTAGTCCTTAGTTGCGCTTGCTATGGCCTCGTCTG
 TGCCGGCTTATCCGAGCATAACTGTGACACCTGATGAAGAGCAAAACTTGAATCATTATATA
 CAAGTTTAGAGAACCTAGTACGAAGTGTCCCTCTGGGGAGCCAGGTGAGAAAAAATC
 TAACTCTCCAAAACATGTTATTCTATAGCATCAAAGGGATCAAATTAAAGGAGCTAGTTA
 CACATGGAGACGCTCACTGAGAATGATGTTAACCAATCCTATCAGTGAAGAAACTACA
 ACTTCCCTACAGGAGGCTTCACACCGAAATAGGAAAGAAAAACACACGGAAAGTACCCC
 ATTCTGGTCGATCAAACCAACAATGTTCCATTGTTGCATGCAGAGGAACCTTATATTG
 AAAATGAAGAGGCCAGGCCAGGCCGGAGCCAGCTGCAAAACAAACTGAGGCACCAAGAATG
 TTGCCAGTTGTTACTGAATCATCTACAAGTCCATATGTTACCTCATACAAGTCACCTGTCAC
 CACTTAGATAAGAGCACTGGCATTGAGATCTACAGAATCAGAAGATGTTCCCTCAGCTCT
 CAGGTGAAACTGCGATAGAAAAACCGAAGAGTTGGAAAGCACCCAGAGAGTTGGAATAAT
 GATGACATTTGAAAAAAATTTAGATATTAATTACAGTGCACAGGCACCTTCTAGTGA
 CACCAGCAACCCAGCATATAGAGAAGATATTGAAGCCTCTAAAGATCACCTAAACGAAGCC
 TTGCTCTAGCAGCAGCAGCAGAACATAAATTAAAAACATGTATAAGTCCAGTTATTGCCA
 GTAGGACGAACAAGTAATAAAATTGATGACATCGAAACTGTTATTACATGCTGTGTAATTG
 TAGATCTAAACTCTATGAATATTAGATATTAAATGTGTTCCACCAGAGATGAGAGAAAAAG
 CTGCTACAGTATTCAATACATTAAAAATATGTGAGATCAAGGAGAGTCACAGCCTTATTA
 AAAGTTTATTAAACAATAATATAAAATTAAACCTACTGATATTCCATAACAAAGCTGA
 TTTAAGCAAAC TGCAATTTCACAGGAGAAATAATCATATTGTAATTCAAAAGTTGTAT
 AAAAATTTCTATTGAGTTCAAATGTGCCAACATCTTATGTGTCATGTGTTATGAACA
 ATTTCATATGCACTAAAAACCTAATTAAAATTTGGTCAGGAAAAAA

FIGURE 146

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68864
><subunit 1 of 1, 350 aa, 1 stop
><MW: 39003, pI: 5.59, NX(S/T): 1
MKPLVLLVALLPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRSPSGEPGREKKSNSPK
HVYSIASKGSKFKELVTHGDASTENDVLNPISEETTFPTGGFTPEIGKKHTESTPFWSI
KPNNVSIVLHAEEPYIENEPEPEPAAKQTEAPRMLPVVTESSSPYVTSYKSPVTTLDK
STGIEISTESEDVPQLSGETAIEKPEEFGKHPESWNNNDILKKILDINSQQQALLSDTSNP
AYREDIEASKDHLKRSLALAAAAEHKLKTMYKSQLLPVGRTSNKIDDIETVINMLCNSRSKL
YEYLDIKCVPPEMREKAATVFNTLKNMCRSRRVTALLKVY
```

Signal peptide:

amino acids 1-19

FIGURE 147

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCACGGCTCCTGCGCCTGAGACAGCTGGCCTG
 ACCTCCAAATCATCCATCCACCCCTGCTGTATCTGTTTCATAGTGTGAGATCAACCCACA
 GGAATATCC**ATG**GCTTTGTGCTCATTGGTTCTCAGTTCTACAGAGCTGGTGTAGGACA
 GTGGCAAGTCACTGGACCGGGCAAGTTGTCCAGGCCTGGTGGGGAGGACGCCGTGTTCT
 CCTGCTCCCTTTCCAGACCAGTGCAGAGGCTATGGAAGTGCAGGTTCTCAGGAATCAG
 TTCCATGCTGTGGTCCACCTCTACAGAGATGGGAAGACTGGGAATCTAACAGATGCCACA
 GTATCGAGGGAGAAGTGAAGGACTCCATTGCAGGGGGCGTGTCTCTAAGGC
 TAAAAAAACATCACTCCCTCGGACATCGGCCTGTATGGGTGCTGGTTCAAGTCCCAGATTAC
 GATGAGGAGGCCACCTGGGAGCTGCAGGCTCACTGGCTCACTCCCTCATTTCCAT
 CGTGGGATATGTTGACGGAGGTATCCAGTTACTCTGCCTGTCCTCAGGCTGGTCCCCCAGC
 CCACAGCCAAGTGGAAAGGTCCACAAGGACAGGATTGTCTTCAGACTCCAGAGCAAATGCA
 GATGGGTACAGCCTGTATGATGTGGAGATCTCATTATAGTCCAGGAAAATGCTGGAGCAT
 ATTGTGTTCCATCCACCTTGCTGAGCAGAGTCATGAGGTGGAATCCAAGGTATTGATAGGAG
 AGACGTTTCCAGCCCTCACCTGGCGCTGGCTTCTATTACTCGGGTTACTCTGTGGT
 GCCCTGTGTGGTGTATGGGATGATAATTGTTCTTCAAATCCAAGGGAAAATCCA
 GGCAGGAACGGACTGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCGGAAACACG
 CAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCCTTCTGATCTGAAA
 ACTGTAACCCATAGAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTACAAGGAA
 GAGTGTGGTGGCTCTCAGGGTTCCAAGCAGGGAGACATTACTGGGAGGTGGACGTGGAC
 AAAATGTAGGGTGGTATGTGGAGTGTGTCGGGATGACGTAGACAGGGGAAGAACAAATGTG
 ACTTTGTCTCCAACAATGGGTATTGGGTCTCAGACTGACAACAGAACATTGTATTTCAC
 ATTCAATCCCCATTATCAGCCTCCCCCCCAGCACCCCTCTACACGAGTAGGGTCTTCC
 TGGACTATGAGGGTGGGACCATCTCCTTCTCAATAACAAATGACCAGTCCCTATTATACC
 CTGCTGACATGTCAGTTGAAGGCTGTTGAGACCCTATATCCAGCATGCGATGTATGACGA
 GGAAAAGGGGACTCCCATATTATGTCAGTGTGCTGGGA**TGA**GACAGAGAACCCCTG
 CTTAAAGGGCCCCACACCACAGACAGCCAGACACAGCCAAGGGAGAGTGTCTCCGACAGGTGGC
 CCCAGCTCCTCTCGGAGCCTGCGCACAGAGAGTCACGCCACTCTCCTTAGGGAGC
 TGAGGTTCTCTGCCCTGAGCCCTGCAAGCAGCAGCGGAGTCACAGCTCCAGATGAGGGGGAT
 TGGCCTGACCTGTGGGAGTCAGAACCCATGGCTGCCCTGAAGTGGGACGGAATAGACTCA
 CATTAGGTTAGTTGTGAAAACCTCCAGCTAACGATCTGAACAAAGTCACAACCTCC
 CAGGCTCCTCATTGCTAGTCACGGACAGTGATTCTGCCTCACAGGTGAAGAGATTAAGAGA
 CAACGAATGTGAATCATGCTTGAGGTTGAGGGCACAGTGTGCTAATGATGTGTTTTA
 TATTATACATTTCCACCATAAACTCTGTTGCTTATTCCACATTAATTACTTTCTCTA
 TACCAAATCACCCATGGAATAGTTATTGAACACCTGCTTGTGAGGCTCAAAGAATAAGAG
 GAGGTAGGATTTCACTGATTCTATAAGCCCAGCATTACCTGATACCAAAACCAGGCAAAG
 AAAACAGAAGAAGAGGAAGGAAAACACAGGTCCATATCCCTCATTAACACAGACACAAAAAA
 TTCTAAATAAAATTAAACAAATTAAACTAAACATATTTAAAGATGATATATAACTACT
 CAGTGTGGTTGTCCACAAATGCAGAGTTGTTAATATTAAATATCAACCAGTGTAAATT
 CAGCACATTAATAAGAAAAAGAAAACCATAAAAAAAAAAAAAAA

FIGURE 148

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866
><subunit 1 of 1, 466 aa, 1 stop
><MW: 52279, pi: 6.16, NX(S/T): 2
MAFVLILVLSFYELVSGQWQVTGPGKVFQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHA
VVHLYRDGEDWESKQMPQYRGRTEFKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEE
ATWELRVAAL GSLPLISIVGYVDGGIQLLCLSSGWFPQOPTAKWKG P Q G Q D L S S D R A N A D G Y
S LYD V E I S I I V Q E N A G S I L C S I H L A E Q S H E V E S K V L I G E T F F Q P S P W R L A S I L L G L L C A L C
G V V M G M I I V F F K S K G K I Q A E L D W R R K H G Q A E L R D A R K H A V E V T L D P E T A H P K L C V S D L K T V T
H R K A P Q E V P H S E K R F T R K S V V A S Q G F Q A G R H Y W E V D V G Q N V G W Y V G V C R D D V D R G K N N V T L S
P N N G Y W V L R L T T E H L Y F T F N P H F I S L P P S T P P T R V G V F L D Y E G G T I S F F N T N D Q S L I Y T L L T
C Q F E G L L R P Y I Q H A M Y D E E K G T P I F I C P V S W G
```

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 131-150, 235-259

FIGURE 149

CCTTCACAGGACTCTCATTGCTGGTGGCA**ATG**ATGTATCGGCCAGATGTGGTGAGGGCTA
 GGAAAAGAGTTGTTGGAACCCCTGGTTATCGGCCTCGTCATCTCATATCCCTGATTGTC
 CTGGCAGTGTGCATTGGACTCACTGTTCAATTATGTGAGATATAATCAAAGAACCTACAA
 TTACTATAGCACATTGTCATTACAACAGACAAACTATATGCTGAGTTGGCAGAGAGGCTT
 CTAACAATTTACAGAAATGAGCCAGAGACTGAAATCAATGGTAAAAATGCATTATAAA
 TCTCCATTAAGGGAAGAATTGTCAAGTCTCAGGTTATCAAGTTCAACAGAACATGG
 AGTGTGGCTCATATGCTGTTGATTGTAGATTCACACTACTGAGGATCCTGAAACTGTAG
 ATAAAATTGTTCAACTTGTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCCTAAAGTA
 GATCCTCACTCAGTAAAATAAAAAAATCAACAAGACAGAACAGACAGCTATCTAAACCA
 TTGCTGCGGAACACGAAGAAGTAAAACCTAGGTAGAGTCTCAGGATCGTTGGTGGACAG
 AAGTAGAAGAGGGTGAATGCCCTGGCAGGCTAGCCTGCAGTGGGATGGAGTCATCGCTGT
 GGAGCAACCTAATTAATGCCACATGGCTTGTGAGTGCTGCTCACTGTTACAACATATAA
 GAACCCTGCCAGATGGACTGCTCCTTGGAGTAACAATAAAACCTCGAAAATGAAACGGG
 GTCTCCGGAGAATAATTGTCCATGAAAATACAAACACCCATCACATGACTATGATATTCT
 CTTGCAGAGCTTCTAGCCCTGTCCTACACAAATGCAGTACATAGAGTTGTCTCCCTGA
 TGCATCCTATGAGTTCAACCAGGTGATGTGATGTTGTGACAGGATTGGAGCACTGAAAA
 ATGATGGTTACAGTCAAAATCATCTCGACAAGCACAGGTGACTCTCATAGACGCTACAAC
 TGCAATGAACCTCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCT
 AGAAGGAAAAACAGATGCATGCCAGGGTACTCTGGAGGACCACTGGTTAGTCAGATGCTA
 GAGATATCTGGTACCTTGCTGGAATAGTGAGCTGGGAGATGAATGTGCGAAACCCAACAAG
 CCTGGTGTAACTAGAGTTACGGCCTGCGGGACTGGATTACTCAAAAACGGTATC**TA**
AGAGACAAAAGCCTCATGGAACAGATAACATTTTTTGTTTTGGGTGTGGAGGCCATT
 TTTAGAGATAACAGAATTGGAGAACAGACTTGCAAAACAGCTAGATTGACTGATCTCAATAAAC
 TGTTGCTTGTGATGCATGTATTCTTCCCAGCTCTGTTCCGCACGTAAGCATTGCTTCTG
 CCAGATCAACTCTGCATCTGTGAGCAATAGTTGAAACTTATGTACATAGAGAAATAGATA
 ATACAATATTACATTACAGCCTGTATTCATTGTTCTCTAGAAGTTGTGAGAATTGAC
 TTGTTGACATAAATTGTAATGCATATATAACAATTGAAAGCACTCCTTTCTTCAGTTCTC
 AGCTCCTCTCATTCAGCAAATATCCATTCAAGGTGCAAGAACAGGAGTGAAAGAAAATA
 TAAGAAGAAAAAAATCCCCTACATTATTGGCACAGAAAAGTATTAGGTGTTTTCTTAGT
 GGAATATTAGAAATGATCATATTCAATTGAAAGGTCAAGCAAAGACAGCAGAACATCAAC
 ACTTCATCATTAGGAAGTATGGAACTAAGTTAAGGAAGTCCAGAAAGAACGCAAGATATA
 TCCTTATTTCATTCCAAACAACTACTATGATAAATGTGAAGAAGATTCTGTTTTGTG
 ACCTATAATAATTACAAACTCATGCAATGTACTTGTCTAAGCAAATTAAAGCAAATAT
 TTATTTAACATTGTTACTGAGGATGTCAACATATAACAATAAAATATAACACCCCA

FIGURE 150

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871
><subunit 1 of 1, 423 aa, 1 stop
><MW: 47696, pi: 8.96, NX(S/T): 3
MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYYSTLSFTTD
KLYAEFGREASNNFTEMSQRLESMVKNAYKSPLREEFVKSQVIKFQQKHGVLAHMLLICR
FHSTEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTL
GQSLRIVGGTEVEEGEWPWQASIQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFG
VTIKPSKMKRGLRIIVHEKYKHPHDYDISLAEELSSPVPYTNAVHRVCLPDASYEFQPGDV
MFVTGFGALKNDGYSQNHLRQAQVTLIDATTNEPQAYNDAITPRMLCAGSLEGKTDACQGD
SGGPLVSSDARDIWYLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKTGI
```

Transmembrane domain:

amino acids 21-40 (type II)

FIGURE 151

GTCGAAGGTTATAAAAGCTTCCAGCAAACGGCATTGAAGTTGAAGATAACAACCTGACAGCA
 CAGCCTGAGATCTTGGGGATCCCTCAGCCTAACACCCACAGACGTAGCTGGTGGATTCCCG
 CTGCATCAAGGCCTACCCACTGTCTCC**ATG**CTGGCTCTCCCTGCCTTGTGGCTCCTGGC
 CGTGACCTTCTTGGTCCCAGAGCTCAGCCCTGGCCCTCAAGACTTGAAGAAGAGGAGG
 CAGATGAGACTGAGACGGCGTGGCCGCTTGCCGGCTGTCCCCCTGCGACTACGACCACGTG
 CGACACCTGCAGGTGCCCTGCAAGGAGCTACAGAGGGTCGGGCCGGCCTGCCTGTGCC
 AGGACTCTCCAGCCCCGCCAGCCGCCGACCCGCCGCATGGGAGAAGTGCACATTGCGG
 CGGAAGAGGGCCGCGCAGTGGTCCACTGGTGTGCCCTCTCCCCGGTCCACTACTGG
 CTGCTGCTTGGGACGGCAGCGAGGCTGCGCAGAAGGGCCCCGCTAACGCTACGGTCCG
 CAGAGCCGAACTGAAGGGCTGAAGCCAGGGGCATTATGTCGTTGCGTAGTGGCCGCTA
 ACGAGGCCGGGCAAGCCGCGTGCCTCAGGCTGGAGGGAGAGGGCCTCGAGGGGCCGACATC
 CCTGCCTTCGGGCCTTGCAGCCGCCTGCGGTGCCGCCAACCCCCGCACTCTGGTCCACGC
 GGCGTCGGGTGGCACGCCCTGCCCTGCTAACGCTGTGCCGCCCTGGTGTGGCACTTCT
 GCCTGCGCGATCGCTGGGCTGCCCGCCGAGCCGCCGAGCCGCAGGGCGCTC**TGA**
 AAGGGGCTGGGCATCTCGGGCACAGACAGCCCCACCTGGGCGCTCAGCCTGGCCCCCG
 GGAAAGAGGAAAACCCGCTGCCTCCAGGAGGGCTGGACGGCGAGCTGGAGCCAGCCCCAG
 GCTCCAGGGCCACGGCGGAGTCATGGTCTCAGGACTGAGCGCTTGTAGGTCCGGTACTT
 GGCGCTTGTTCCTGGCTGAGGTCTGGGAAGGAATAGAAAGGGCCCCAATTTTTTTTA
 AGCGGCCAGATAATAATAATGTAACCTTGCAGGGTTAAAAAAAAAAAAAAA

FIGURE 152

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68874
><subunit 1 of 1, 238 aa, 1 stop
><MW: 25262, pI: 6.44, NX(S/T): 1
MLGSPCLLWLLAVTFLVPRAQPLAPQDFEEEEADETETAWPPLPAVPCDYDHCRHLQVPCKE
LQRVGPAACLCGPLSSPAQPPDPPRMGEVRIAEEGRAVVHWCAPFSPVLHYWLLLWDGSEA
AQKGPPNATVRRAELKGLKPGGIYVVCVVAANEAGASRVPQAGGEGLEGADIPAFGPCSRL
AVPPNPRTLVHAAVVGVTALALLSCAALVWHFCLRDRWGCPRAAARAAGAL
```

Important features of the protein:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 194-220

N-glycosylation site.

amino acids 132-135

FIGURE 153

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCCGAAGAAGTTCC
 CTGCCCCGATGAGCCCCGCGTGCCTCCCCACTATCCCAGGCAGGGCTGGGCACCGGG
 CCCAGCGCCGACGATCGCTGCCGTTTGCCCTGGAGTAGGATGTGGTCAAAGGATGGGC
 TTCTCCCTAACGGGCTCACAAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGCTGCCTGCT
 CTACGCCCTCAATCTGCTCTTGGTTAATGTCCATCAGTGTGGCAGTTCTGCTTGG
 TGAGGGACTACCTAATAATGTTCTCACTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTC
 ATTTGACTTACTTCTGTGGTTCATCCGGTCATGATTGCTGTTGCTGTTCTTATCAT
 TGTGGGGATGTTAGGATATTGTGGAACGGTAAAAGAAATCTGTGCTTCTGCATGGTACT
 TTGGAAGTTGCTTGTCAATTCTGTGTTAGAACTGGCTGTGGCAGTGGACATATGAAACAG
 GAACTTATGGTCCAGTACAATGGTCAGATATGGTCACTTGAAGGCCAGGATGACAAATTA
 TGGATTACCTAGATATCGGTGGCTTACTCATGCTTGAATTTCAGAGAGAGTTAAGT
 GCTGTGGAGTAGTATATTCACTGACTGGTGGAAATGACAGAGATGGACTGGCCCCAGAT
 TCCTGCTGTGTTAGAGAATTCCCAGGATGTTCAAACAGGCCACCAGGAAGATCTCAGTGA
 CCTTATCAAGAGGGTGTGGGAAGAAAATGTATTCTTTGAGAGGAACCAAACAACTGC
 AGGTGCTGAGGTTCTGGGAATCTCCATTGGGGTGACACAAATCTGGCATGATTCTCACC
 ATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCCTGGGACAGACCAAATGATGTC
 CTTGAAGAATGACAACCTCAGCACCTGTATGTCCTCAGTAGAACTGTTGAAACCAAGCC
 TGTCAAGAATCTTGAACACACATCCATGGCAAACAGCTTAATACACACTTGAGATGGAG
 GAGTTATAAAAAGAAATGTCACAGAAGAAAACCACAAACTGTTTATTGAGACTTGTGAATT
 TTTGAGTACATACTATGTGTTCAGAAATATGTAGAAATAAAATGTTGCATAAAATAACA
 CCTAAGCATATACTATTCTATGCTTAAAATGAGGATGAAAAGTTCATGTCATAAGTCAC
 CACCTGGACAATAATTGATGCCCTAAAATGCTGAAGACAGATGTCATACCACTGTGTAGC
 CTGTGTATGACTTTACTGAACACAGTTATGTTGAGGCAGCATGGTTGATTAGCATTT
 CGCATCCATGCAAACGAGTCACATATGGTGGACTGGAGCCATAGTAAAGGTTGATTACTT
 CTACCAACTAGTATATAAGACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATA
 ACTTTATTACTCAGCGATCTATTCTGTATGCTAAATAAAATTATATCAGAAAACCTTC
 AATATTGGTGAACACATTGTCTTAAGCTGATCAGGGATTGGTATATAAGTCTGTGTTAAA
 GAGCAAGCTAACACATTGTCTTAAGCTGATCAGGGATTGGTATATAAGTCTGTGTTAAA
 TCTGTATAATTCACTGCGATTTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAA
 ATTTGTCCTGTATAGCATCATTATTTAGCCTTCTGTTAATAAGCTTACTATTCTGT
 CCTGGGCTTATATTACACATATAACTGTTATTAAATACTTAACCACTAATTTGAAAATTA
 CCAGTGTGATACATAGGAATCATTATTCAAGAATGTTAGTCTGGTCTTGGAGTATTAATAA
 GAAAATTGACATAACTTAGTTGATTCAAGAAAGGACTGTATGCTGTTTCTCCAAATG
 AAGACTCTTTGACACTAACACTTTAAAAGCTTATCTTGCCCTCTCCAAACAAGAA
 GCAATAGTCTCCAAGTCATATAAAATTCTACAGAAAATAGTGTCTTTCTCCAGAAAAT
 GCTTGTGAGAATCATTAAACATGTGACAATTAGAGATTCTTGTGTTATTCACTGATTA
 ATATACTGTGGCAAATTACACAGATTATTAATAATTGTTACAAGAGTATAGTATATT
 GAAATGGAAAAGTGCATTACTGTATTGTGTTATTCTCAGAATATGGAA
 AGAAAATTAAATGTCATATAATTCTAGAGAGTAA

FIGURE 154

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880
><subunit 1 of 1, 305 aa, 1 stop
><MW: 35383, pI: 5.99, NX(S/T): 0
MAREDSVKCLRCLLYALNLLFWLMSISVLAWSAWMRDYLNNVLTLTAETRVEEAVILTYFPV
VHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQ
WSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMWDPPDSCCVREF
PGCSKQAHQEDLSLDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWAL
YYDRREP GTDQMMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL
```

Signal peptide:

amino acids 1-33

Transmembrane domains:

amino acids 12-35, 57-86, 94-114, 226-248

FIGURE 155

GAGAGAGGCAGCAGCTGCTCAGCGACAAGGATGCTGGCGTGAGGGACCAAGGCCTGCC
 TGCACTCGGGCCTCCAGCCAGTGCTGACCAGGGACTCTGACCTGCTGCCAGCCAGGA
 CCTGTGTGGGAGGCCCTGCTGCCCTGGGTGACAATCTCAGCTCAGGCTACAGGGAG
 ACCGGGAGGATCACAGAGCCAGC**ATG**TACAGGATCCTGACAGTGTCAACCTCTGAACAGC
 CTCGATGTCAAACCCCTGCGCAAACCCGTATCCCCATGGAGACCTCAGAAAGGTGGGAT
 CCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGTGGTGCCTCATCAAGG
 TGATTCTGGATAAATACTACTTCCTCTGCGGGCAGCCTCTCCACTTCATCCGAGGAAGCAG
 CTGTGTGACGGAGAGCTGGACTGTCCCTGGGGAGGACGAGGAGCACTGTGTCAAGAGCTT
 CCCCAGGGCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGG
 ACTCGGCCACAGGAACTGGTTCTGCGCTGTTGACAACACTCACAGAACGCTCGCTGAG
 ACAGCCTGTAGGCAGATGGCTACAGCAGAGCTGTGGAGATTGGCCAGACCAGGATCTGGA
 TGTTGTTGAAATCACAGAAAACAGCCAGGAGCTCGCATGCGAACTCAAGTGGCCCTGTC
 TCTCAGGCTCCCTGGCTCCCTGCACTGTCTGCCTGTGGAAAGAGCCTGAAGACCCCCCGT
 GTGGTGGGTGGGGAGGAGGCCTCTGTGGATTCTTGGCCTTGGCAGGTCAAGCATCCAGTACGA
 CAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGTCCTCACGGCAGCCCAC
 GCTTCAGGAAACATACCGATGTGTTCACTGGAAGGTGCGGGCAGGCTCAGACAAACTGGC
 AGCTTCCCACCCATGGCTGTGGCAAGATCATCATCATTGAATTCAACCCATGTACCCCAA
 AGACAATGACATGCCCTCATGAAGCTGCAGTCCCACACTTCTCAGGCACAGTCAGGC
 CCATCTGTCTGCCCTTTGATGAGGAGCTCACTCCAGCCACCCACTCTGGATCATTGGA
 TGGGGCTTACGAAGCAGAATGGAGGGAAAGATGTCTGACATACTGCTGCAGGCGTCAGTCCA
 GGTCATTGACAGCACCGTGCAATGCAGACGATGCGTACCAAGGGGAAGTCACCGAGAAGA
 TGATGTGTGCAGGCATCCCGAAGGGGTGTGGACACCTGCCAGGGTACAGTGGTGGGCC
 CTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATCGTTAGCTGGGCTATGGCTGCC
 GGGCCCGAGCACCCAGGAGTATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATG
 TCTGGAAGGCTGAGCTG**TAAT**GCTGCTGCCCTTGCACTGCTGGAGCCGCTCCCTCCTG
 CCCTGCCACCTGGGATCCCCAAAGTCAGACACAGAGCAAGAGTCCCCTGGTACACCC
 CTCTGCCACAGCCTCAGCATTCTGGAGCAGCAAAGGGCTCAATTCTGTAAGAGACCC
 TCGCAGCCCAGAGGCGCCAGAGGAAGTCAGCAGCCCTAGCTCGGCCACACTGGTGTCCC
 AGCATCCCAGGGAGAGACACAGCCCACCTGAACAAGGTCTCAGGGTATTGCTAAGCCAAGAA
 GGAACCTTCCCACACTACTGAATGGAAGCAGGCTGTCTGAAAAGCCCAGATCACTGTGGG
 CTGGAGAGGAGAAGGAAAGGGTCTGCCAGCCCTGCGTCTCACCCATCCCCAAGCCTA
 CTAGAGCAAGAACCAAGTTGTAATATAAAATGCACTGCCACTGTGGTATGACTACCGTT
 ACCTACTGTTGTCATTGTTATTACAGCTATGCCACTATTATAAGAGCTGTGTAACATCT
 CTGGCAAAAAAA

FIGURE 156

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68885
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47644, pI: 5.18, NX(S/T): 2
MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIALLSLASIIVVVLIKVILDKYF
LCGQPLHFIPRKQLCDGEELDCPLGEDEEHCVKSFPPEGPAVAVRLSKDRSTLQVLDSATGNWF
SACFDNFTEALAETACRQMGYSRAVEIGPDQDLDVVEITENSQELRMRNSSGPCLSGSLVSL
HCLACGKSLKTPRVVGGEASVDSWPWQVSIQYDKQHVCGGSILDPHWLTAHCFRKHTDV
FNWKVRAGSDKLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFD
EELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPE
GGVDTQCQGDSGGPLMYQSDQWHVVGIVSWGYZGCZGPSTPGVYTKVSAYLNWIYNVWKAEL
```

Transmembrane domain:

amino acids 32-53 (typeII)

FIGURE 157

GGGCTGAGGCAGTGAGAGACCGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGCATCCCCAGGCTCCAG
 AGCTCCCTGGTACAGTCTGTGGCTGAGCAATGGCCCTCCCAGCCCTGGGCTGGACCCCTGGAGGCTCCTGGGCC
 TTTTCCTCTCCAAGTCTCAGCTGCTGCTGCCGACGACGCCGGGGAGGCAGGGCCAGGGGCCATGCCA
 GGGTCAGATACTATGCAGGGATGAACGTAGGGACTTAGCTTCCACCAGAAGGGCTCCAGGATTTGACA
 CTCTGCTCTGAGTGGTATGAAATACTCTACGTGGGCTCGAGAACGCATTCTGGCTTGGATATCCAGG
 ATCCAGGGTCCCCCAGGCTAAAGAACATGATAACCGTGGCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTA
 AGAAGAAGAGCAATGAGACACAGTGTTCAACTTCATCCGTGTCCTGGTTCTTACAATGTCACCCATCTAC
 CCTGCGGCACCTTCGCCTCAGCCCTGCTTACCTCATTGAACCTCAAGATCCTACCTGTTGCCCATCTCGG
 AGGACAAGGTATGGAGGGAAAAGGCCAAAGCCCTTGACCCGCTCACAGCATAACGGTGTCTGGTGGATG
 GGATGCTTACTTCTGGTACTATGAACAACTTCCTGGCAGTGAGCCATCCTGATGCGCACACTGGGATCCCAGC
 CTGCTCTCAAGACCGACAACCTCCCTCGCTGGCTGCATCATGACGCCCTTGTGGCAGGCATCCCTCGACCC
 AGGTCGTCTACTTCTTCGAGGAGACAGCAGCGAGTTGACTTCTTGAGAGGCTCCACACATCGGGGTGG
 CTAGAGTCTGCAAGAACATGACGTGGCGGGCAAAGCTGCTGCAGAAGAAGTGGACCACCTCTGAAGGCCAGC
 TGCTCTGCACCCAGCCGGGCAGCTGCCCTCAACGTATCCGCACCGGTCTGCTCCCCGCCATTCTCCA
 CAGCTCCCCACATCTACGCACTTCCAGTGGCAGGTTGGCAGGACCAGGAGCTGCGGTTGTGCCT
 TCTCTCTTGGACATTGAACGTCTTAAGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA
 CTTATAGGGCCCTGAGACCAACCCCGGCCAGGCAGTTGCTCAGTGGCCCTCCTGATAAGGCCCTGACCT
 TCATGAAGGACCATTCTGATGGATGAGCAAGTGGTGGGACGCCCTGCTGGTAAATCTGGGTGGAGTATA
 CACGGCTTCAGTGGAGACAGCCCAGGGCTTGATGGCACAGCCATCTGTATGTACCTGGAACCAACACAG
 GGTCGCTCCACAAGGCTGTGGTAAGTGGGACAGCAGTGCTCATCTGGTGAAGAGATTGAGCTGTTCCCTGACC
 CTGAACCTGTTGCAACCTGCACTGGCCCCACCCAGGGTGCAGTGTTGTAAGGCTCTCAGGAGGTGTCTGGA
 GGGTGCCTGGAGCCAAGTGTAGTGTCTATGAGAGCTGTGACTGTGCTTGCCTGGGACCCCCACTGTGCCT
 GGGACCCCTGAGTCCCAGACCTGTTGCCTCTGTGCCCTGGGACCCCCACTGTGCCT
 GGAACCCAGAGTGGCATGTGCCAGTGGCCATGAGCAGGAGCCTCGGCCTCAGAGCCCGCAAATCATTA
 AAGAACGTCCTGGCTGCCCCAACCTCCATCTGGAGCTCCCTGCCCTCACCTGTCAGCCTGGCTCTTATTATT
 GGAGTCATGCCAGCAGCAGTCCCAGAACGCTCTTCACTGTCTACAATGGCTCCCTTGCTGATAGTGCAGG
 ATGGAGTTGGGGTCTCTACCAAGTGTGGCAACTGAGAATGGCTTTCATACCTGTGATCTCTACTGGTGG
 ACAGCCAGGACCAGACCCCTGCCCTGGATCTGAACACTGGCAGGCATCCCCGGAGCATGTGAAGGTCCCGTTGA
 CCAGGGTCAGTGGTGGGCCCTGGCTGCCAGCAGTCTACTGGCCCTACTTGTACTGTACTGTCT
 TTGCCTTAGTGCTTCAAGGAGCCCTCATCATCTCGTGGCTCCCTATTGAGAGCAGTCCGGCTCGGGCAAGG
 TTCAGGGCTGTGAGACCCCTGCCCTGGGAGAAGGCCCTGTTAACGAGAGCAACACCTCCAGTCTCCCAAGG
 AATGCAGGACCTGCACTGGCAGTGTGGACGCTGACAACAACACTGCCTAGGCAGTGAGGTAGCTTAAACTCTAGGCA
 CAGGCCGGGGCTGCCAGGACCCATGGCTGGCAGGACACTGGCAGTGGCTGGCAGGCCAAGCAGCAGCCCTGACTAGGATGACAG
 CAGCACAAAAGACCACTTCTCCCTGAGAGGAGCTTGTCTACTCTGCATCACTGATGACACTCAGCAGGGTG
 ATGCACAGCAGTCTGCCCTCCCTATGGACTCCCTCTACCAAGCAGCATGAGCTCTCTAACAGGGTGGGGCTAC
 CCCAGACCTGCTCTACACTGATATTGAAGAACCTGGAGAGGATCCTCAGTCTGGCCATTCCAGGGGCCCTC
 CAGAAACACAGTGTTCAGAGAGACCCCTAAAAAACCTGCCCTGGCAGGACCCATGGTAATGAACACCAACACTC
 TAAACAAATCATATGCTAACATGCCACTCCTGAAACACTCCACTCTGAAGCTGCCCTTGGACACCAACACTCC
 TCTCCCAAGGGTCACTGCAAGGGATCTGCTCCCTCTGCTTCCCTTACCAAGTGTGCAACCGCTGACTCCAGGAAGTC
 TTTCCCTGAAGTCTGACCACTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTCTGCCCTGGCAGAATGG
 CAGGGGTAATCTGAGCCTCTTCACTCCCTAACCTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTCTTGT
 TTGGGATTGAGAAAATGCTTGTCAGAGACTGTTATTTTATTAAAAATAAGGCTTAAAAAA

FIGURE 158

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71166
><subunit 1 of 1, 761 aa, 1 stop
><MW: 83574, pi: 6.78, NX(S/T): 4
MALPALGLDPWSLLGLFLFQLLQLLLPTTAGGGGQGPMPRVRYAGDERRALSFFHQKGLQ
DFDTLLLSDGNTLYVGAREAILALDIQDPGVPRLNIMIPWPASDRKKSECAFKKKSNETQC
FNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDPAHKHTA
VLVDGMLYSGMTMNNFLGSEPILMRTILGSQPVLKTDNFLRWLHHDASFVAAPSTQVVYFFF
ETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLPFNVIRHAVLL
PADSPTAPIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTYRGPET
NPRPGSCSVGPSSDKALTFMKDHFLLMDEQVVGTPLLVKSGVEYTRLAVETAQGLDGHSHLV
YLGTTTGSILHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTOQAVFVGFSGGVWRVPRAN
CSVYESCVDCVLARDPHCAWDPESTCCLLSAPNLNSWKQDMERGNPEWACASGPMSRSLRP
QSRPQIIKEVIAVPNSILELPCPHLSALASYWSHGPAAVPEASSTVYNGSLLLIVQDGVGG
LYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWP
HFVTVTVLFALVLSGALIIILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRT
SASDVADNNCLGTEVA
```

Signal peptide:

amino acids 1-30

Transmembrane domains:

amino acids 136-156, 222-247, 474-490, 685-704

FIGURE 159

AGGGTCCCTAGCCGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTCCGTAGAAG
 TGAGCATGGCTGGGCAGCGAGTGCTTCTTAGTGGGCTTCCTCCCTGGGGTCTGCTC
 TCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGA
 CCGGGTTCTCAGATTCTCAAGATCACGGTCATAATGTCACCATGCTAACCAACAAAAGAG
 GTCCTTTATGCCAGATTTAAAAAGGAAGAAAATCATATCAAGTTATCAGTGGCTTGCA
 CCTGAAGATCATCAAAGAGAATTAAAAAGAGTTGATTCTTCTGGAAGAAACTTATTAGG
 TGGCAGAGGAAAATTGAAAACCTATTAAATGTTCTAGAATACTTGGCCTGAGTGCAGTC
 ATTTTTAAATAGAAAGGATATCATGGATTCTTAAAGAATGAGAACTTCGACATGGTGATA
 GTTGAACACTTTGACTACTGTCCTTCTGATTGCTGAGAAGCTGGGAAGCCATTGTGGC
 CATTCTTCCACTTCATTGGCTCTTGAATTGGCTACCAATCCCCTGTCTATGTT
 CAGTATTCCGTTCTGCTGACTGATCACATGGACTCTGGGGCGAGTGAAGAATTCTG
 ATGTTCTTAGTTCTGCAGGAGGAAACAGCACATGCAGTCTACATTGACAACACCATAA
 GGAACATTACAGAAGGCTCTAGGCCAGTTGTCTCATCTTACTGAAAGCAGAGTTGT
 GGTCATTAACACTGACTTGCCTTGATTTGCTGACCTCTGCTTCCAAACACTGTTAT
 GTTGGAGGCTTGATGGAAAAACCTATTAAACCAGTACCACAAGACTTGGAGAACTTCATTG
 CAAGTTGGGACTCTGGTTTGTCCCTGTGACCTGGCTCCATGGTGAACACCTGTCAGA
 ATCCGAAATCTCAAGGAGATGAACAATGCCCTTGCTCACCTACCCCAAGGGGTGATATGG
 AAGTGTCACTGTTCTCATTGCCAAAGATGTCACCTGGCTGCAAATGTGAAAATGTGGA
 CTGGCTTCTCAGAGTGACCTCTGGCTACCCAAGCATCCGTCTGTTGTCACCCACGGCG
 GGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTCCCCATGGTGGGATCCCTCTCTT
 GGAGACCAGCCTGAAAACATGGTCCAGTAGAAGCCAAAAGTTGGTGTCTATTGAGT
 AAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGAT
 ACAAGTCCGGCAGTGGCTGCCAGTGTCACTCTGCGCTCCACCGCTCAGCCCCACACAG
 CGGCTGGTGGGCTGGATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTA
 TGTCTTCAGCAGCCCTGGCATGAGCAGTACCTGTTGACGTTTGTGTTCTGCTGGGGC
 TCACTCTGGGACTCTATGGCTTGTTGTTGAAGAACAGGAAAATGCCAAAATCATCCTTCACTG
 TAATTGCTACAAATTCACTCCTACTAGCTCCTGCCTGCTAGCAGAAATCTTCCAGTCCT
 CTTGTCCTCCTTGTTGCCATCAGCAAGGGCTATGCTGTGATTCTGCTCTGAGTGACTTG
 GACCACTGACCCCTCAGATTCCAGCCTTAAACACCTTCTCATGCGCCTCTCCGAA
 TCACACCCCTGACTCTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCACTCCTGCC
 TACTATCTATCATGGAATAACATCCAAGAAAGACACCTGTCATAITCTTCAGTTCTGTT
 TGTTCTCCCACATATTCTCTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTGAGG
 CGGACACAGGCTCACAGGTCTCCACATTGGGCTCCATGGTGCCTGCTGGTCCCCACAGT
 TCTGGCTGAGCAGGCATGGAGACTGTAGGTTCCAGATTCCTGAAAAATAAAAGTTACA
 GCGTTATCTCTCCCCAACCTCACTAA

FIGURE 160

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71169
><subunit 1 of 1, 523 aa, 1 stop
><MW: 59581, pI: 8.68, NX(S/T): 1
MAGQRVLLVGFLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGNVTMLNHKRGP
FMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQCSHF
LNRKDIDSLKNENFDMVIVETFDYCPFLIAEKLGKPVAILSTSFGSLEFGLPIPLSYVPV
FRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHLLLKAELWF
INSDFAFDFARPLLPNTVYVGGILMEKPIKPVQPQDLENFIAKFGDSGFVLVTLGSMVNCTCQNP
EIFKEMNNAFAHLPQGVIWKCQCSHWPKVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQ
NSIMEAIQHGVPVMVGIPLFQGDQOPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYK
SAAVAASVILRSHPPLSPTQRLVGWIDHVLTGGATHLKPYVFQQPWHEQYLFDVVFVLLGLT
LGTLWLCGKLLGMAVWWLRGARKVKET
```

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 483-504

FIGURE 161

GGGCTGTTGATTGTGGGGATTTGAAGAGAGGGAGGAATAGGAGGAAGGGGTTGAGGGGCT
 GCCTCTGGCATATGCACACACTCACACATTCTGTACACCCGTACACACACATACCATGTT
 CTCCATCCCCCAGGTCCAGGCCCTCAGTGTGTCAGGCCATCCAGCAGGGCTACCCCTGAAGCTCT
 GGCTGCAGCCCTCCGTCCAGTGGCAGGCAGGCTTCATCCCTCCTTCTCTCCAAAGCCCA
 ACTGCTGTCACTGCATGCTGCCAAGGAGGAGGGAACTGCAGTGACAGCAGGAGTAAGAGT
 GGGAGGCAGGACAGAGCTGGACACAGGTATGGAGAGGGGTTAGCGAGCCTAGAGAGGGC
 AGACTATCAGGGTGCAGGGCGGTGAGAATCCAGGGAGAGGAGCGGAAACAGAAGAGGGGAGA
 AGACCGGGGCACTGTGGTTGCAGAGCCCCTCAGCC**ATG**TGGGAGCCAAGCCACACTGGC
 TACCAGGTCCCCAACAGTCCCAGGCTGCCCTGGTTCTGGTCTGGCCCTGGGGCC
 GGGTGGGCCAGGAGGGTCAGAGCCCCTGCTGGAGGGGAGTGCCTGGTGGTCTGTGA
 GCCTGGCCGAGCTGCTGCAGGGGGCCGGGGAGCAGCCCTGGAGAGGCACCCCTGGG
 GAGTGGCATTGCTGCGGCCGAAGCCACCCATGAGCCAGCAGGGAAACCGGCAATGGC
 ACCAGTGGGCCATCTACTCGACCAGGTCTGGTGAACGAGGGCGGTGGCTTGACCGGGC
 CTCTGGCTCCTTCGTAGCCCTGTCAGGGGTGCTACAGCTCCGGTTCCATGTGGTGAAGG
 TGTACAACCGCAAACACTGTCAGGTGAGCCTGATGCTGAACACGTGGCCTGTCACTCAGCC
 TTTGCCAATGATCCTGACGTGACCCGGAGGCAGCCACCAGCTGTGCTACTGCCCTTGG
 CCCTGGGGACCGAGTGTCTGCGCTGCGTCGGGGAAATCTACTGGTGGTGGAAATACT
 CAAGTTCTCTGGCTCCTCATCTCCCTCT**TGA**GGACCCAAAGTCTTCAGCACAAGAAT
 CCAGCCCTGACAACCTTCTGCCCCAGAAACAGCAGAGGCAGGAGAGAG
 ACTCCCTCTGGCTCCTATCCACCTTTGCATGGACCCCTGTGCCAACACCCAAAGTTAA
 GAGAAGAGTAGAGCTGTGGCATCTCCAGACCCAGGCTTCCACCCACCCACAGTTACC
 CTCCCAAGCCACCTGCTGCATCTGTTCTGCCTGCAGCCCTAGGATCAGGGCAAGGTTGGCA
 AGAAGGAAGATCTGCACTACTTGCGGCCCTGCTCCTCCGGTCCCCACCCAGCTTCT
 GCTCAATGCTGATCAGGGACAGGTGGCGCAGGTGAGCCTGACAGGCCCCCACAGGAGCCCAG
 ATGGACAAGCCTAGCGTACCCCTGCAGGCTTCTCCTGTGAGGAAGGCCAGCATCAGGATC
 TCAGCCAGCACCGTCAGAACGCTGAGCCAGCACCGTATGGCTAGGGTGGAGGCTAGCCAC
 AGGCAGAAGGTGGAGGGCCTGGAGTCTGTTGCTGGAGGAAGGAAGGAGGGTGTATTG
 TCTAGACTGAACATGGTACACATTCTGCATGTATAGCAGAGCAGCCAGCAGGTAGCAATCCT
 GGCTGTCTTCTATGCTGGATCCCAGATGGACTCTGGCCCTTACCTCCCCACCTGAGATTAG
 GGTGAGTGTGTTGCTCTGGCTGAGAGCAGAGCTGAGAGCAGGTATACAGAGCTGGAAGTGG
 ACCATGGAAAACATCGATAACCAGCATCCTCTGCTTGGCACCTCTGAAACTGCTCCAC
 CTTTGAAGTTGAACCTTAGTCCCTCCACACTCTGACTGCTGCCCTCTCCAGCTCTC
 TCACTGAGTTATCTTCACTGTACCTGTTCCAGCATATCCCCACTATCTCTCTTCTGAT
 CTGTGCTGTCTTATTCTCCCTTAGGCTTCTATTACCTGGGATTCCATGATTCAATTCTT
 CAGACCCCTCTCCAGTATGCTAAACCCCTCCCTCTCTTCTTATCCGCTGCCCCATT
 GGCCAGGCTGGATGAATCTATCAATAAAACAATAGAGAATGGTGGTCAGTGAGACACTAT
 AGAATTACTAAGGAGAAGATGCCTCTGGAGTTGGATCGGGTGTACAGGTACAAGTAGGTA
 TGTTGCAGAGGAAAATAATCAAACGTATACTAAATTAAAAA

FIGURE 162

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180
><subunit 1 of 1, 205 aa, 1 stop
><MW: 21521, pI: 7.07, NX(S/T): 1
MLGAKPHWLPGPLHSPGLPLVLVLLALGAGWAQEGSEPVILLEGECLVVCEPGRAAAGGPGGA
ALGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEGGGFDRASGSFVAPVRGVY
SFRFHVVKVYNRQTVQVSMLNTWPVISAFANDPDVTREAATSSVLLPLDPGDRVSLRLRRG
NLLGGWKYSSFSGFLIFPL
```

Signal peptide:

amino acids 1-32

FIGURE 163

GCTGTTCTCTCGGCCACCACTGGCCGCCGGCGCAGCTCCAGGTGTCTAGCCGCCAGC
 CTCGACGCCGTCCCGGGACCCCTGTCTCGCGAAGCCCTGGCCCCGGGGCCGGGCAT
 GGGCCAGGGCGGGGTGAAGCGGCTTCCCAGGGCGTGAATGGCGGGCTTCAGCC**AT**
GAAGACCCCTCATAGCCGCCTACTCCGGGTCTCGCGCGAGCGTCAGGCCAGGCTGACC
 GGAGCCAGCGCTCTCACGGAGGACCTCGCCTGCGCGAGGGCTGGGAGATGGGGACT
 GGATCCAGCATTCTCCGCCCTCCAGGACCTTCTGTACCTGGCTCAATAGGTCAA
 GGTGGAAAAGCAGCTACAGGTATCTCAGTGCTCCAGTGGTCTGTCTTGTACTGG
 GAGTGGCCTGCAGTGCATCCTCATGTACATATTCTGCACTGATTGCTGGCTATCGCTGTG
 CTCTACTTCACGGCTGGTGTGGCGTACTTCGAGACTACTTCCATCCAGCTGGTGA
 GTGGGTCCGAAACTGGGCTGTGTGGCGTACTTCGAGACTACTTCCATCCAGCTGGTGA
 AGACACACAACCTGCTGACCACCAAGGAACATATCTTGGATACCACCCCCATGGTATCATG
 GCCCTGGGTGCCTCTGCAACTTCAGCACAGAGGCCACAGAAGTGAGCAAGAAGTCCCAGG
 CATAACGGCCTTACCTGGCTACACTGGCAGGCAACTCCGAATGCCTGTGTTGAGGGAGTACC
 TGATGTCTGGAGGTATCTGCCCTGTCAAGCCGGACACCATAAGACTATTTGCTTCAAAGAAT
 GGGAGTGGCAATGCTATCATCATCGTGGTGGGGTGCAGCTGAGCTCTGAGCTCCATGCC
 TGGCAAGAATGCAGTCACCCCTGCGGAACCGCAAGGGCTTGTGAAACTGCCCTCGTCATG
 GAGCTGACCTGGTCCCCTACTCCTTGGAGAGAATGAAGTGTACAAGCAGGTGATCTTC
 GAGGGAGGCTCTGGGCCATGGTCCAGAAGAAGTCCAGAAATACATTGGTTCGCCCC
 ATGCATTTCCATGGTCGAGGCCTCTCTCCGACACCTGGGGCTGGTGCCTACTCCA
 AGCCCATCACCACGTGTTGGAGAGGCCATCACCACCCAGCTGGAGCACCCAACCCAG
 CAAGACATCGACCTGTACCATGTACATGGAGGCCCTGGTGAAGCTTCGACAAGCA
 CAAGACCAAGTCGGCCTCCGGAGACTGAGGTCTGGAGGTGAAC**TGA**GCCAGCCTCGGG
 GCCAATTCCCTGGAGGAACCAGCTGCAAATCACTTTTGCTGTAAATTGGAAGTGTCA
 TGGGTGTCTGTGGTTATTAAGAAATTATAACAATTTGCTAAACCAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAA

FIGURE 164

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184
><subunit 1 of 1, 388 aa, 1 stop
><MW: 43831, pi: 9.64, NX(S/T): 3
MKTLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGSSIILSALQDLFSVTWLNR
KVEKQLQVISVLQWVLSFLVLGVACSAIIMYIFCTDCWLIAVLYFTWLVDWNTPKKGGRS
QWVRNWAVWRYFRDYFPIQLVKTHNLLTRNYIFGYHPHGIMGLGAFCNFSTEATEVSKKFP
GIRPYLATLAGNFRMPVLREYLMGGICPVSRTIDYLLSKNGSGNAIIVVGAAESLSSM
PGKNAVTLRNRKGFKLALRHGADLVPIYSFGENEVYKQVIFEEGSWGRVQKKFQKYIGFA
PCIFHGRGLFSSDTWGLVPYSKPITTVVGEPIТИPKLEHPTQQDIDLYHTMYMEALVKLFDK
HKTKFGLPETEVLEVN
```

Important features of the protein:

Transmembrane domain:

amino acids 76-97

N-glycosylation sites.

amino acids 60-63, 173-176, 228-231

N-myristoylation sites.

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-245, 318-323, 378-383

FIGURE 165

GGGCGGCCGGATGGGGCCGGGGCGGCCGCACTCGCTGAGGCCCGACGCAGGCCGGCCGGCC
 GGGCGAGGAGCGCGGGCGCCAGAGCAGGGCGGAGGCGACGCCGGGACGCCCGCGACGAGCAGGTGGCG
 GCGGCTGCAGGCTTGTCAGCCGAAGCCCTGAGGGCAGCTGTTCCCCTGCTGACCTTGTGCCTTGGA
 CGGCTGCTCTCAGCGAGGGCGTGCACCCGCTCCTGAGCAGGCC**TG**GGCCTGCTGCCCTGAAGACCCA
 GTCGTGCTGCACCTGCTGGCTGGCTTGTCTGGTGAAGTGGCTGGTCAACTCGTCCAGCTGTGCAC
 GCTGGCGCTGGCCGGTCAAGCAAGCAGCTCACCGCCCTCAACTGCCGCTCGCCTACTCACTCTGGAGCCA
 ACTGGTCATGCTGGAGTGGCTGCACGGAGTGTACACTGTTACGGACCAGGCCACGGTAGAGCGCTT
 TGGGAAGGAGCACGAGTCATCATCCTCAACCACAACCTCGAGATCGACTTCCTCTGTGGGTGGACCATGTGTGA
 GCGCTTGGAGTGCTGGGAGCTCCAAGGTCTCGTAAGAAGGAGCTGCTACGTGCCCTCATGGCTGGAC
 GTGGTACTTCTGGAGATTGTGTTCTGCAAGCGGAAGTGGGAGGAGGCCACCGTGGTGAAGGGCTGAG
 GCGCCTGCGACTACCCCGAGTACATGTGGTTCTCCTGACTGCCAGGGACGCCCTCACGGAGACCAAGCA
 CCGCGTTAGCATGGAGGTGGCGGCTGCTAACGGGCTTCCTGCTCAAGTACCACTGCTGCCGCGACCAAGGG
 CTTCACCACCGCAGTCAAGTGCCTCCGGGGACAGTCGAGCTGTCTATGATGTAACCTGAACCTCAGAGGAAA
 CAAGAACCGTCCCTGCTGGGATCCTCACCGGAAGAAGTACGAGGCCACATGTGCGTGAAGGAGATTCCCTCT
 GGAAGACATCCCGCTGGATGAAAGGAAGCAGCTCAGTGGCTCATAAACTGTACCAAGGAGACCGCCTCCA
 GGAGATATAATCAGAACGGCATGTTCCAGGGAGCAGTTAACGCTGCCGGAGGCCGTGGACCCCTCTGAA
 CTTCCGTCCCTGGGCCACCATTCCTGCTCCCCCTTCAGTTGTCTGGCGTCTTGCCAGGGATCACC
 TCTCCTGATCCTGACTTCTGGGTTGTGGAGCAGCTCCCTGGAGCTGAGACTGATAGGAGAATCGCT
 TGAACCTGGGAGGTGGAGATTGCA**TG**GCTGAGATGGCATCACTGACTCCAGCCTAGGCAACAGAGCAAGACT
 CAGTCTAAAAAAAAAAAAACAAAAACCCAGAAATTCTGGAGTTGAACCTGTGAGTTACTGACATGAAAA
 ATTCACTAGAGGCTGAACAGCAGATTGAGCAGGAGAAAAATCAGCAAGCTTGAAGATGGTACCTGAGATT
 TTTCAGGCTAATGAAAAAGAATGAAGGAAATTAAACAGCCTCAGAGACCCATGGTCACCGTCACACAAATCAA
 CATATGCATGATGAGACTCCAGAACAGGAGAGAGAAAGGGTCAGAAAGAATGCCACAAGCTGATGAAAAACA
 GTAACCTACCCACTCAGGAAGCTCAGTGAACCTAACATGAGGATGAATATCAGAGATCCACACCTAGATATTCAT
 AATCAAAGTGTCAAATGACAAAGAATCTGAAAGCAGCAAGAGATGAGCAACTATCTTGTCAAAGGATCTTG
 ATCAGATTAACAGCTCATTCTCCTCAGAAATCATGGGAGCCAGGGAGATGTGGGATGAACACTGTTGAAGGCAA
 AACCTCAACTGTAATTATTGGACTTTGAGCTTAGATGGCCTGACCTCTTGTCTTCAGGGACAGTTTCA
 ATTAATCCCTAATAACAATTAGTCAGCTTGGGAGGCCAGACGGGTGGATCATTTGGGTCAGGCTGATCTCAAACCTCCT
 TTACACCTGTAATCCAGCAGCTTGGGAGGCCAGACGGGTGGATCATTTGGGTCAGGCTGATCTCAAACCTCCT
 GAGTTCAGGTGATCTGCCGCTCAGCCTCCAAAGTGTGATTGCAAGCGTGAGCCACTGCCCTGGCCGGA
 ATTTCTTTAAGGCTGAATGATGGGGGCCAGGCACGATGGCTCACGCCGTGATCCAAAGTAGCTGGATTGTA
 AACATGCACCAACATGCCCTGGCTAATTTGTATTTAGTAGAGACGTGTTAGCCAGGCTGGCTCGATCTCCT
 GACCTCAAGTGACCACTGCCCTCAGCCTCCAAAGTACTGGGATTACAGGCGTGAGCCACTGTCCTGGCCTTGA
 GCATCTTGTGATGTGCTTATTGGCATTGTATATCTTCTATCTTGGGAAATGTCGTTCAAGTCCTTGT
 CCTTTAAATTTTATTATTATTATTGAGACAGGGCTTGTGTTCTGGCCAGGCTGGAGTA
 CAGTGGCACAGTCTGGCTCACTGCAGCCTGCCAGCTGGCTGAGTGTGATCTCCACCCACTCAGCCTCCCTGT
 AGCTGTATTGGTGTAGCTGTAGTTGTATTTGTGAGCAGGAGACAGCATTCAACCATGA
 TGCCCAAGGCTGGCTTGAACTCCTGAGCTCAAGTGATCTGCCCTGCTCAGCCTCCAAAGTGTGGGATTACAGA
 CATGAGCCACTGCACCTGGCAAACCTCCAAAATTCAACACACACACACACACACACACACACACACACACAC
 GAGGGGCCGGTGTGGCCCAACTACCAGGGAGACTGAAGTGGGAGGATCGCTGGGATGAGAAGTCGAGGCTG
 CAGTGAGTCGAGGTTGTGCGACTGCATTCCAGCCTGGACAACAGAGTGAGACCCCTGTCT

FIGURE 166

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213
><subunit 1 of 1, 368 aa, 1 stop
><MW: 42550, pI: 9.11, NX(S/T): 1
MGLLAFLKTQFVLHLLVGFVFVSGLVINFVQLCTLALWPVSKOLYRRLNCRLAYSLWSQLV
MLLEWWSCTECTLFTDQATVERFGKEHAVIILHNFEIDFLCGWTMCERFGVLGSSKVLAKK
ELLYVPLIGWTWYFLEIVFCKRKWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRFTETKHR
VSMEVAAAKGLPVILKYHLLPRTKGFTTAVKCLRGTVAAVDVTLNFRGNKNPSLLGILYGKK
YEADMCVRRFPLEDIPIDEKEAAQWLHKLYQEKDALQEIYNQKGMFPGEQFKPARRPWTLLN
FLSWATILLSPLFSFVLGVFASGSPLLILTFLGFVGAASFVRRRLIGESLEPGRWRLQ
```

Important features of the protein:

Signal peptide:

amino acids 1-25

Transmembrane domains:

amino acids 307-323, 335-352

Tyrosine kinase phosphorylation sites.

amino acids 160-168, 161-169

FIGURE 167

GATATTCTTATTTAAGAACATGAAAGTACTATGCATCACTCCCTCCAATGTCCTGGGGCA
 GCCACCAGGCATATTCATCTTGTGTGTTTCTTGCTTAGCACTGGGCACCTCTT
 GCTTATTCTTGGTAGGAAAGGGCTCAGTTGTCTGGGGTTGGCAGGCAGGCCG
 GCTTACGCCGTGATAACGCCCTGGGTTAGAAGGGAAGGAAAGATAAAACTTTATACAAATGGG
 GATAGCTGGGTCTGAGACCTGCTCAGTAAAATCCTGGATCTGCCTATACCTCTT
 TTCTCTAACCTGGCATACCCGCTAAAGCCTCTCAGGGCTCTCTGTTCTAGGATCAA
 AGTATTAGAGCTACAAGAGCCCTCATGGTCTGGCCCCCTGCCCTGGCCAGCTTCATTGT
 ACATGTGGTGTCTCTTGTGTTCTGTAATGTGGTATGCCATGGGTCTTGACAAAGCCT
 TTCCTTTGGCTGGACACTGTTCCCTGCCCTACTCTCCTACTTAATATGTAGTC
 ATCCTGCAGATTCAATTCTAACATCATTCTCCAGGGATCCTGCCCTGACAGAATCTCAT
 CTTGTTAATGCTCTCATAAGACCCTTGTTCCCTTGCAGCACCTGCCACTCAGTTGTA
 TCTTATGTGCGTTGTGGGTATGGGTGTCTGTTCCCCAGAATGCCAGCTCTGAGC
 TCGGTGAGGGTCAAGGCATTGCTGTGCCCTGCCAGGTATAGTGCCTACATGTGGTGGTGCT
 CATGTTTAGAGACTAAATGGAGGAGGAGATGAGGAAAAGATTGAAATCTCTCAGTCACCA
 GATGGGTAGGGCCCAGCATTGTAATTACACGTTGACTGTGCTGTGAATTATCTGGGGA
 TGCAGGTCTGATTCACTAGGCCAGGTTGGCATCTCTAACAAACTCCCACGTGATGCTGA
 TGCTGGCCTATGAACTATACTAAATAGTAAGAACATCTATGGAGCCAGGCTGGCATGGTGGC
 TCACACCTATGATCCCAGCACTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATT
 TCAAGACTAGCCTGGCAACATGGTGGAACCCATCTGACTAAAAACACAAATTAGCTG
 GGCATGGTGGCACATGCCTGTAGTCCCAGCTACTTGGGAGGCTGAAGCAAGAGAACGCTTG
 AACCTGGGAGGCGGAGGTTGCAGTGAGCCGAGATCAGGCCACTGTATTCCAACCAGGGTGAC
 AGAGTGAGACTCTATGTCCAAAAAAAAAAAAAA

FIGURE 168

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234
><subunit 1 of 1, 143 aa, 1 stop
><MW: 15624, pi: 9.58, NX(S/T): 0
MHSLQCPGAATRHIHLCVCFALALGHFLLISLVGKGLSLSGVGGRQAGLRLIRPWRR
EGKINFYTNNGDSWGLRPASSVKFLGSAYTFFSLTWHTLLKASQGFSLFLGSKYLELQEPSWS
GPPGQLHCTCGVLLSFL
```

Important features of the protein:

Signal peptide:

amino acids 1-28

FIGURE 169

GGCTGGACTGGAACTCCTGGTCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGA
 TTATAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACTTTCAGCAACTAAAAAGCCAC
 AGGAGTTGAAC TGCTAGGATTCTGACT**ATG**CTGTGGTGGCTAGTGCTCCTACTCCTACCTAC
 ATTAAAATCTGTTTTGTTCTTGTAACTAGCCTTACCTCCTAACACAGAGGATCTGT
 CACTGTGGCTCTGGCCAAACCTGACCTCAC TCTGGAACGAGAACAGAGGTTCTACCCAC
 ACCGTCCCCTCGAAGCCGGGACAGCCTCACCTGCTGGCCTCTCGCTGGAGCAGTGCCCTC
 ACCAACTGTCTCACGTCTGGAGGC ACTGACTCGGGCAGTAGCAGGTAGCTGAGCCTTGGTA
 GCTGCGGCTTCAAGGTGGCCTTGCCTGGCGTAGAAGGGAT**TGA**CAAGCCGAAGATT
 CATAGGCGATGGCTCCACTGCCAGGCATCAGCCTGCTGTAGTCAATCACTGCCCTGGGG
 CCAGGACGGCGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCACGCTGCCGCCAT
 CTAACCTTTCATGTCCCTGCACATCACCTGATCCATGGGCTAATCTGAACCTGTCCCAAGG
 AACCCAGAGCTTGAGTGAGCTGGCTCAGACCCAGAAGGGGTCTGCTTAGACCACCTGGTT
 TATGTGACAGGACTTGCATTCTCCTGGAACATGAGGGAACGCCGGAGGAAGCAAAGTGGCA
 GGGAAAGGAAC TTGTGCCAAATTATGGGT CAGAAAAGATGGAGGTGTTGGTTATCACAAGGC
 ATCGAGTCTCCTGCATT CAGTGGACATGTGGGGAAAGGGCTGCCGATGGCGATGACACACT
 CGGGACTCACCTCTGGGCCATCAGACAGCCGTTCCGCCCGATCCACGTACAGCTGCTG
 AAGGGCAACTGCAGGCCATGCTCATCAGCCAGGCAGCAGCCAAATCTGCGATCACCAG
 CCAGGGCAGCGTCTGGAAAGGAGCAAGCAAAGTGACCAAGGCTTCCCTCCCTCCCTC
 TGAGAGGCCCTCCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGCTAATG
 GCTCAGTGTGGCCAGGAGGT CAGCAAGGCCTGAGAGCTGATCAGAAGGGCTGCTGTGCG
 AACACGGAAATGCCCTCAGTAAGCACAGGCTGCAAAATCCCCAGGCAAAGGACTGTGTGGCT
 CAATTAAATCATGTTCTAGTAATTGGAGCTGCCCCAAGACCAAAGGAGCTAGAGCTTGGT
 TCAAATGATCTCCAAGGGCCCTTATAACCCAGGAGACTTGATTGAATTGAAACCCCCAA
 TCCAAACCTAAGAACCCAGGTGCATTAAGAACATCAGTTATTGCCGGGTGTGGCTGCTGTAATG
 CCAACATTGGGAGGCCAGGCAGGGTAGATCACCTGAGGT CAGGAGTTCAAGACCCAGCCTG
 GCCAACATGGT GAAACCCCTGTCTACTAAAAAATACAAAAAAACTAGCCAGGCATGGTGGT
 GTGTGCCTGTATCCCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTGAAACCTGGGAGGT
 GAAGGAGGCTGAGACAGGAGAATCACTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGA
 AAAAATAAAAAAAGAATTATGGTTATTGTAA

FIGURE 170

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277
><subunit 1 of 1, 109 aa, 1 stop
><MW: 11822, PI: 8.63, NX(S/T): 0
MLWWLVLLLPTLKSVFCSLVTSLYLPNTEDSLWLWPKPDLHSGTRTEVSTHTVPSKPGTA
SPCWPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRD
```

Signal peptide:

amino acids 1-15

FIGURE 171

GCGGGCCCGCGAGTCCGAGACCTGTCCCAGGAGCTCCAGCTCACGTGACCTGTCACTGCCTC
CCGCCGCCTCCTGCCCGGCCATGACCCAGCCGGTCCCCGGCTCTCCGTGCCGCGCT
GGCCCTGGGCTCAGCCGCACTGGCGCCGCCCTGCCACTGGCCTCTTCCGGGGAGGCGGT
GCCCCCCATGGCGAGGCCGGCGAGAGCAGTGCTGCTGCTCCCCCGAGGACAGCCGCTGTGG
CAGTATCTCTGAGCCGCTCCATGCAGGGAGCACCCGGCGTGCAGACGCTGAGGCTGCTGAC
CCTGGAGCAGCCGCAAGGGGATTCTATGATGACCTGCGAGCAGGCCAGCTTGGCCAACC
TGGCGCGGCTCATCCAGGCCAAGAACGGCGCTGGACCTGGCACCTCACGGCTACTCCGCC
CTGGCCCTGGCCCTGGCGCTGCCGCCGGACGGCGCGTGGTACCTGCGAGGTGGACGCGCA
GCCCGGAGCTGGACGGCCCTGTGGAGGCAGGCCGAGGCGAGCACAGATCACCTCC
GGCTGAAGCCGCCCTGGAGACCCCTGGACGAGCTGCTGGCGCGGGGAGGCCGGCACCTTC
GACGTGGCGTGGTGGATGCGGACAAGGAGAACTGCTCCGCCTACTACGAGCGCTGCCGTGCA
GCTGCTGCGACCCGGAGGCATCCTGCCGTCCAGAGTCCTGTGGCGCGGGAAAGGTGCTGC
AACCTCCGAAAGGGGACGTGGCGGCCAGTGTGCGAACCTAAACGAACGCATCCGGCGG
GACGTCAAGGGTCTACATCAGCCTCCTGCCCTGGCGATGGACTCACCTGGCCTCAAGAT
CTAGGGCTGGCCCTAGTGAGTGGCTCGAGGGAGGGTTGCCTGGGAACCCAGGAATTGAC
CCTGAGTTTAAATTGAAAATAAGTGGGCTGGGACACAAAAAAA

FIGURE 172

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71282
><subunit 1 of 1, 262 aa, 1 stop
><MW: 28809, pI: 8.80, NX(S/T): 1
MTQPVPRLSVPAAALALGSAALGAAFATGLFLGRRCPWRGRREQCLLPEDSRLWQYLLSRS
MREHPALRSLRLLTLEQPQGDSMMTCEQAQLLANLARLIQAKKALDLGTFTGYSALALALAL
PADGRVVTCEVDAQPPELGRPLWRQAEAEHKIDLRLKPALETLDELLAAGEAGTFDVAVVDA
DKENCSAYYERCLQLLRPGGILAVLRLWRGKVLQPPKGDVAAECVRNLNERIRRDVRVYIS
LLPLGDGLTLAFKI
```

Important features of the protein:

Signal peptide:

amino acids 1-25

Transmembrane domains:

amino acids 8-30, 109-130

N-glycosylation site.

amino acids 190-193

Tyrosine kinase phosphorylation site.

amino acids 238-246

N-myristoylation sites.

amino acids 22-27, 28-33, 110-115, 205-210, 255-260

Amidation sites.

amino acids 31-34, 39-42

FIGURE 173

CCGCCGCCGAGCCGCTACCGCCGCTGCAGCCGTTCCGGCCTGGCCTCTGCCGTCA
GCATGCCACACGCCCTCAAGCCCAGGGACTTGGTGTGCTAAGATGAAGGGCTACCC
 TGGCCTGCCAGGATCGACGACATCGCGATGGCGCGTGAAGCCCCACCCAACAAGTACCC
 CATCTTTTCTTGGCACACACGAAACAGCCTCCTGGGACCCAAAGGACCTTCCCTACG
 ACAAAATGTAAAGACAAGTACGGGAAGCCAACAAGAGGAAAGGCTTAATGAAGGGCTGTGG
 GAGATCCAGAACAAACCCCCACGCCAGCTACAGCGCCCTCCGCCAGTGAGCTCCTCCGACAG
 CGAGGCCCGAGGCCAACCCGCCAGGCAGTGACGCTGACGAGGACGATGAGGACCGGG
 GGGTCATGGCGTACAGCGGTAAACGCCACAGCTGCCAGCAGAGGATGGAGAGCGACTCA
 GACTCAGACAAGAGTAGCGACAACAGTGGCTGAAGAGGAAGACGCCGCTGCCCTAAAGATGTC
 GGTCTCGAAACGAGCCCAGAACGGCCTCCAGCGACCTGGATCAGGCCAGCGTGTCCCCATCCG
 AAGAGGAGAACTCGGAAAGCTCATCTGAGTCGGAGAACGACAGCGACCAGGACTTCACACCT
 GAGAAGAAAGCAGCGGTCCGGCGCCACGGAGGGGCCCTGGGGGGACGGAAAAAAAAGAA
 GCCGCCGTCAAGCTCCGACTCCGACTCCAAGGCCGATTGGACGGGCCAGCCTGAGCCGG
 TGGCCATGGCGCGGTGGCTCCTCCCTCCCTCTCCCTCCCTCCGACTCCGATGTG
 TCTGTGAAGAACGCTCCGAGGGGCAGGAAGCCAGCGGAGAACGCTCTCCGAAGCCCGAGG
 GCGGAAACCAGCCTGAACGCCCTCCGTCCAGCTCAGCTGACAGTGAACAGCGACGAGG
 TGGACCGCATCAGTGAGTGGAAAGCGGGGGACGAGGCGGGAGGCAGGCTGGAGGGCCGG
 CGCGGGCGAGAGCAGGAGGAGCTGCGGCGCCTGCGGGAGCAGGAGAACGGAGGAGAACG
 GCGGAGGCGCGAGCGGGCCGACCGCGGGAGGCTGAGCGGGGAGCAGCGGGAGCAGCGGGG
 ACGAGCTCAGGGAGGAGCAGTGAGCCCTCAAGAACGGGGACGCAAGGGCCGGGGCGGG
 CCCCCGTCCCTCTGACTCCGAGCCCGAGGCCAGCTGGAGAGAGAGGCCAAGAAATCAGC
 GAAGAACGCCAGTCCTCAAGCACAGAGCCGCCAGGAAACCTGCCAGAACGGAGAACGAG
 TGCGGCCCGAGGAGAACAGCAAGCCGTGAAGGTGGAGCGGACCCGAAGCGGTCC
 GAGGGCTTCGATGGACAGGAAGGTAGAGAACAGAACGGCCCTCCGTGGAGGAGAACG
 GCAGAACGCTGCACAGTGAGATCAAGTTGCCCTAAAGGTCGACAGCCGGACGTGAAGAGGT
 GCCTGAATGCCCTAGAGGAGCTGGGAACCCCTGCAGGTGACCTCTCAGATCCTCCAGAAC
 ACAGACGTGGTGGCACCTTGAAGAACAGATTGCCGTTACAAGCGAACAGACGTAATGGA
 GAAGGCAGCAGAACAGTCTATAACCGGCTCAAGTCGCGGGCCTCGGCCAACAGATCGAGGCG
 TGCAGAAAGTGAACAAGGCTGGATGGAGAACGGAGAACGGCGAGGAGAACGCTGGCCGGGAG
 GAGCTGGCCGGGGAGGAGGCCAGGAGAACGGCGGAGGACAAGCCCAGCACCCTC
 AGCCCCAGTGAATGGCGAGGCCACATCACAGAACGGGGAGAGCGCAGAGAACGGAGCACG
 AGGAGGGTCGGACTCGGAGGAGGGCCAAGGTGTGGCTCCTCTGAAGACCTGCACGACAGC
 GTACGGGAGGGTCCGACCTGGACAGGCCCTGGAGCGACCGGGAGCAGCGAGAGGGCAGC
 GGGGGACTCGGAGGCCCTGGACAGGAGAGCT**TGA**GCCGCCGGCAGCCAGGCCAGCCCCGC
 CCGAGCTCAGGCTGCCCTCTCCTCCGGCTCGCAGGAGAGCAGAGCAGAGAACGAGA
 AACGCTGTGCTGTTGTATTGTTCCCTGGGTTTTTCTGCCTAATTCTGTGATT
 TCCAACCAACATGAAATGACTATAAACGGTTTTAATGA

FIGURE 174

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286
><subunit 1 of 1, 671 aa, 1 stop
><MW: 74317, pi: 7.61, NX(S/T): 0
MPHAFKPGDLVFAKMKGYPHWPARIDDIADGAVKPPPNKYPPIFFFGTHETAFLGPKDLPYD
KCKDKYGKPNKRKGNEGLWEIQNNPHASYSAPPVSSSDSEAPEANPADGSDADEDDEDRG
VMAVTAVTATAASDRMESDSDSDKSSDNSGLRKTPALKMSVSKRARKASSLDQASVSPSE
EENSESSSESEKTSQDFTPEKKAAVRAPRRGPLGGRKKKAPSASDSKADSDGAKPEPV
AMARSASSSSSSSSSDDVSVKKPRGRKPAEKPLPKPRGRKPKPERPPSSSSDSDSDEV
DRISEWKRDEARRRELEARRRREQEEELRLREQEKEEKERRERADRGEAERGSGGSSGD
ELREDDEPVKKRGRKGRGRGPPSSSDSEPEAELEREAKKSAKKPQSSSTE PARKPGQKEKRV
RPEEKQQAKPVKVERTRKSEGFSMDRKVEKKKEPSVEEKLQKLHSEIKFALKVDSPDVKRC
LNALEELGTLQVTSQILQKNTDVVATLKKIRRYKANKDVMKAEEVYTRLKSRLGPKIEAV
QKVNKAGMEKEKAEEKLAGEELAGEEAPQEKAEDKPSTDLSAPVNGEATSQKGESAEDKEHE
EGRDSEEGPRCGSSEDLHD SVREGPD LDRPGSDRQERERARGDSEALDEES
```

Signal peptide:

amino acids 1-13

FIGURE 175

GTGGTTCTGGATCTCACCTTACCAACTGCAGATCTGGGACTCATCAGCCTCAATAATTATTAATTAAATTA
 ACACCATTGAAAGAGAACATTGTTTCATC**A**TGAATGCTAATAAAGATGAAAGACTTAAAGCCAGAAGCCAAGA
 TTTCACCTTCTGCTTGTGATGCTAAGCATGACATGTTCTTCAAGCTACTGGCACTTTGAAGCA
 AAAATTCCAAGACTCAAGCTAACCTACAAAGACTTGTGCTTCAATAGCTGATTCCCTTTGGGTTCATC
 AGAAGGACTGGATTTCAAACTCTCTTAGATGAGGAAAGAGGCAGGCTGCTCTGGAGCCAAAGACCACAT
 CTTCTACTCAGTCTGGTACTAAACAAAATTAAAGAAGATTATTGGCTGCTGCAAAGGAACGGGTGGA
 ATTATGTAATTAGCTGGAAAGATGCCAATACAGAAATGTCAAATTCTACAGAGTACTTCAGCCCTATAACAA
 AACTCACATATGTGTGAACTGGAGCATTCTACATCCAAATATGGGTATTGATCTGGAGTCTACAAGGA
 GGATATTATTCAAACACTACACATAATTGGAGTCTGGAGACTGAAATGTCCTTCGATCCTCAGCAGCC
 TTTGCTCAGTAATGACAGATGAGTACCTCTACTCTGAAACAGCTCTGATTCTGGAAAGATACTGCATT
 CACTCGATCCCCTGGGCTACTCATGACCACACTACAGAACTGACATTTCAGAGCACTACTGGCTCAATGG
 AGCAAAATTATTGAAACTTCTACACCAGACACCTACAATCCAGATGATGATAAAATATATTCTCTTCG
 TGAATCATCTCAAGAAGCAGTACCTCCGATAAAACCATCCTTCTGAGTTGAAAGAGTTGTAAGAATGATGT
 AGGAGGACAACGCGCTGATAAAACAAGTGGAGCATTCTTAAGGCCAGACTGATTGCTCAATTCTGGAAAG
 TGATGGGCAGATACTTACTTGATGAGCTCAAGATATTATTACTCCCCACAAGAGATGAAAGAAATCCTGT
 AGTATATGGAGTCTTACTACAACCGCTCCATCTCAAAGGCTGCTGTTGTGTGATAGCATGGCTGACAT
 CAGAGCAGTTTAATGGCCATATGCTCATAAGGAAAGTGCAGACCATGTTGGGTGAGTATGATGGGAGAAT
 TCCTTATCCACGGCTGGTACATGTCCAAGCAAAACCTATGACCCACTGATTAAGTCCACCCGAGATTTCAGA
 TGATGTCATCAGTTCATAAAGCGGACTCTGTGATGTATAAGTCGTATACCAGTTGCAAGGAGGACAAACGTT
 CAAGAGAATCAATGTGGATTACAGACTGACACAGATAGTGGGATCATGTCATTGCAAGAGATGGCAGTACGA
 TGTAATGTTCTGGAACAGACATTGAACTGTCCTCAAAGTGTGAGCATTTCAAGGAAAAGTGGAAATATGGA
 AGAGGTAGTGTGGAGGAGTTGAGATATTCAAGCACTCATCAATCATCTGAAACATGGAATTGTCTGAAAGCA
 GCAACAATTGTACATTGGTCCCGAGATGGATTAGTTCAGCTCTCCTGACAGATGCGACACTTATGGGAAAGC
 TTGCGCAGACTGTTGCTTGCAGAGACCCACTGTGCTGGGATGGAAATGATGTCATTGCTCCTGATATGCTCCTAC
 TTCTAAAAGGAGAGCTAGACGCCAAGATGAAAAATATGGCAGCCAAATCACCAGTGTGCTGGGACATCGAAGACAG
 CATTAGTCATGAAACTGCTGATGAAAAGGTGATTTGGCATTGAAATTAACTCAACCTTCTGGAATGTATACC
 TAAATCCCAACAGCAACTATTAAATGGTATATCCAGAGGTCAAGGGGATGAGCAGTCAGAGGAGTTGAAAGCCCGA
 TGAAAGAATCATCAAAACGGAATATGGCTACTGATTGCAAGTTGCAAGAAGGATTCTGGGATGTATTACTG
 CAAAGCCCAGGAGCACACTTCATCCACACCATAGTGAAGCTGACTTGAATGTCATTGAGAATGAAACAGATGGA
 AAATACCCAGAGGGCAGAGCATGAGGAGGGCAGGTCAAGGATCTATTGGCTGAGTCACGGTTGAGATACAAAGA
 CTACATCCAAATCTTAGCAGCCAAACTTCAGCCTCGACCAGTACTGCGAACAGATGTGGCACAGGGAGAAGCG
 GAGACAGAGAAACAAGGGGGCCCAAAGTGGAAAGCACATGCAAGGAAATGAAAGAAGAAACGAAATCGAAGACATCA
 CAGAGACCTGGATGAGCTCCCTAGAGCTGTAGCCACG**TAG**TTTCTACTTAATTAAAGAAAAGAATTCTTAC
 TATAAAACATTGCCTCTGTTGTATATCCCTATAGTAATTCTACATAATGCTTCCATGGAGTTGCTAAGG
 CACAAGACAATACTGAAATAAGACAATATGTGATGAATATAAGAAAGGGCAAAAATTCTGAAACCAGTTT
 CCAAGAACAAATCTGCACAAGCAAAGTATAAGAATTATCCTAAAAATAGGGGTTACAGTTGAAATGTTTA
 TGTTTGAGTTGGAATTATTGTCATGAAATAGTGGAGCTAAGCAAGCCCCGAATTGATAGTGTATAAGGT
 GCTTATTCCCTCGAATGTCATTAAGCATGGAATTTCACCATGCACTGCTATGTTCTATGAAACAGATATA
 CATTCTATTGAGAACCAAGCTACCTTGTGGTAGGAAATAAGAGGTCAAGACACAAATTAGACAAACTCCATTATC
 AACAGGAACCTCTCAGTGAGCCATTCACTCTGGAGAATGGTATAGGAATTGGAGAGGTGCAATTCTTCT
 TGGCCACTGGGTTAAATTAGTGTACTACACATTGATTACTGAAAGGGCACTAATGTTCCCCCAGGATTCT
 ATTGACTAGTCAGGAGTAACAGGTACAGAGAGAAGTGGTCTAGTTATGTGTTTTAGAGTATATACTAA
 GCTCTACAGGGACAGAAATGCTTAATAAATACTTTAATAAGATATGGAAAATATTAAATAAAACAAGGAAAACA
 TAATGATGTATAATGCATCTGATGGGAAGGCATGAGATGGGATTGTTAGAAGACAGAAGGAAAGACAGCCAT
 AAATTCTGGCTTGGGAAAACATATCCCCTGAAAAGGAAGAACATCACAATAAAAGTGGAGAGTAATGTA
 TGGAGCTTTCACTAGGGTATAAGTAGCTGCCAATTGTAATTCTCATCTGTTAAAAAAATCTAGATTATAACA
 AACTGCTAGCAAAATCTGAGGAAACATAAATTCTCTGAAAGAATCATAGGAAGAGTAGACATTGTTATAACC
 AATGATATTCTCAGTATATATTCTCTCTTTAAAAAATTATTCATACTCTGTATATTATTCTTTACTGC
 CTTTATTCTCCTGTATATTGGATTGATTATTTGAGTGAATAGGGAGAAACAAATATATAACACACAGA
 GAATTAAAGAAAATGACATTCTGGGAGTGGGATATATTGTTGAATAACAGAACAGAGTGTAAAATTAAAC
 AACGGAAAGGGTAAATTAAACTCTTGACATCTCACTCAACCTTCTCATTGCTGAGTTAATCTGTTGTAATT
 GTAGTATTGTTTGTAAATTAAACAATAAAAGCCTGCTACATGT

FIGURE 176

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883
><subunit 1 of 1, 777 aa, 1 stop
><MW: 89651, pI: 7.97, NX(S/T): 3
MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLQNIPLRKLTYKDLNNNSCIPFL
GSSEGLDFQTLLLDEERGRLLLGAKDHIFLSLVDLNKNFKKIYWPAAKERVELCKLAGKDA
NTECANFIRVLQPYNKTHIYVCGTGAHPICGYIDLGVYKEDIIIFKLDTHNLESGRLKCPFD
PQQPFASVMTDEYLYSGTASDFLGKDTAFTRSLGPTHDHYIRTDISEHYWLNGAKFIGTFF
IPDTYNPDDDKIYFFFRESSQEGSTSDFKTIISRVGRVCNDVGGQRSLINKWTTFLKARLIC
SIPGSDGADTYFDELQDIYLLPTRDERNPVVYGVFTTSSIFKGSAVCVYSMADIRAVFNGP
YAHKESADHRWVQYDGRIPYPRPGTCPSKYDPLIKSTRDFPDDVISFIKRHSVMYKSVYPV
AGGPTFKRINVVDYRLTQIVVDHviaEDGQYDVMFLGTDIGTVLKVVSIKEKWNMEEVLEEL
LQIFKHSSIILNMELSLKQQQLYIGSRDGLVQLSLHRCDTYGKACADCCLARDPYCAWDGNA
CSRYAPTSKRRARRQDVKYGDPITQCWDIEDSISHTADEKVIFGIEFNSTFLECIPKSQQA
TIKWYIQRSGDEHREELKPDERIIKTEYGLLIRSLQKKDSGMYYCKAQEHTFIHTIVKLTLN
VIENEQMENTQRAEHEEGQVKDLLAESRLRYKDYIQILSSPNFSLDQYCEQMWHREKRRQRN
KGGPKWKHMQEMKKRNRRHRLDELPRAVAT
```

Important features of the protein:**Signal peptide:**

amino acids 1-36

N-glycosylation sites.

amino acids 139-142, 607-610, 724-727

Tyrosine kinase phosphorylation site.

amino acids 571-576

Gram-positive cocci surface proteins 'anchoring' hexapeptide.

amino acids 32-37

FIGURE 177

CCCTGACCTCCCTGAGCCACACTGAGCTGGAAGCCGCAGAGGTCATCCTGGAGCATGCCAACCGCGGGGAGCAGA
 CAACCTCCCAGGTAAGCTGGAGCAAGACTGAAGCTTCTTCAGGAGCCTGGTGTATTTCCCCCACCCAC
 CTCAGCAGTTCAGCCAGCAGGGACTGATCAGGTGTCTGGAGCTGGGAGCAGAAGGGTGGCTGGCAAGA
 GTGGCCTGGAGAAAGAGGTTCAAGCCTTGACCAGCCAGCTGCCGTACTACAAGATCCAGAACCATGGGCATC
 GGGTAGGGTGGGGGGCACAGGTGTATGTCACAGGGAGGGAAAGGTATTAAAGGTAACAGTGTGGCACAATAGTTAA
 AGCCATTGAGGGTGTATGGAGCTACAGAGGGAGGGAAAGGTATTAAAGGTAACAGTGTGGCACAATAGTTAA
 GAGCACAGTTTGGAGCTAGACCGACATAGGTTCAAATCTCTCTGTGCTCCTAGTCTGTAGCCCCAGGT
 AAGGGAGTGACTTAACCTCTGGACTTCATACTAAAGTAGGGCAATAATAGCACCCACCTCAT
 AGGGAGATAAATGACATAATGTATGT**A**TGCAACTAGCAAAGTACCAAGTCCCATAGTAAGTCATGCCACAG
 TATTCCACCCACCCCTGTTCTGCCTCCAAACCAGGTACTGCAACGACTGGAGCAGAGCGGAGCAGGCTT
 CAGAGCGGGAGGCTCAAGCATAGAACAGAGGTTACAGGAAGTGCAGAGAGCATCCGCCGGCACAGGTGAGCC
 AGGTGAAGGGGCTGCCCGCTGGCCCTGCTGCAGGGGCTGGCTTAGATGTGGAGCGCTGGCTGAAGCCAGCCA
 TGACCCAGGCCAGGATGAGGTGGAGCAGGAGCGCGGCTCAGTGAGGCTCGGCTGTCCCAGAGGGACCTCTC
 CAACCGCTGAGGATGCTGAGCTTCTGACTTGAGGAATGTGAGGGAGCAGGGAGAGCTTTGAGGAGCCTGCC
 CCCAACCCCTGGCACGAGGCCCTCCCCTGCCCTGCACACGTGGTATTCGCTATCAGGCAGGGCGTAGGATG
 AGCTGACAATCACGGAGGGTGAGTGGCTGGAGGTATAGAGGAGGGAGATGCTGACGAATGGTCAAGGCTCGGA
 ACCAGCACGGCAGGTAGGTTGTCCTGAGCGATATCTCAACTTCCCGACCTCTCCCTCCAGAGAGCAGCC
 AAGACAGTGACAATCCCTGCGGGGAGGCCACAGCATTCTGGCACAGGCCCTGTACAGCTACACCGGACAGA
 GTGCAGAGGGAGCTGAGCTCCCTGAGGGGCACTCATCCGCTGCTGCCCGGCCAACAGATGGAGTAGATGACG
 GCTTCTGGAGGGAGAATTGGGGCGTGTGGGGTCTTCCCTCCCTGCTGGAGAGCTGCTGGCAAGGCTGCTGGCCCC
 CAGGGCCACCTGAACCTCTGACCCCTGAACAGATGCTGCCGCTCCCTCTCCAGCTCTCCACCTGCAC
 CTACCTCTGTGTTGGATGGGCCCCCTGCACCTGTCCTGCCTGGGACAAAGGCTGGACTTCCCTGGGTTCTGG
 ACATGATGGCACCTGACTCAGGCCGATGCGTCCACCACCTCCCCCGCCGGCTAAAGCCCGGATCTGGCCACC
 CAGATCCCCTCAC**T**GAAGGCCAGGAAAGCCTGACCCCCAGTGATGCTGCTGCCCTATCTCAAGCTGTCA
 CCACACCATCAATGATCCAGAGCAACACAGCCAAAAGCTGGAATGCCCTTATTCACCCCTCACCTCCAGGGT
 GGAAACTTGCCCTTCCATTCTAGAGCTGGAACCCACTCCTTTTTCCATTGTTCTATCATCTTAGGACC
 GGAACTACTACCTCTCTGTGACTGACCCCTATCTAGGGTGGTGAATGCTGAAATCTGGGCTGGAAAC
 ATTCATCAAGGTCTCTAGTAGTTCTGGCCACCTCTTCCCACCTGGCTCCATGACCCACCCACTCTGGATG
 CCAGGGTCACTGGGTTGGCTGGGAGAGGAACAGGCCCTGGGAATCAGGAGCTGGAGCAGGATGCGAAGCAG
 CTGTAATGGCTGAGCGGATTATTGACAATGAATAAAGGGCACGAAGGCCAGGCCAGGGCTGGCCTTGTG
 CTAAGAGGGCAGGGGGCTACGGTGTATTGCTTAGGGCCCACACGGGCAGGGCCTGCTCCAGTGCAC
 GCTCTATCATATGGAGCGAGGTGTGGGGAGGGCGGGCAGGCAGCCCTGTTGCAAGGCAGGGGAAGGAGAAGAGAC
 TGAGGGGCTGTGACCTCTCTGAGGCCCCCAGCCTGAGACTGTGCAACTCCAGGTGGAGTAGAGCTGGCCCTC
 AGCTGGGGGGCAGTGCTGTCAGTGGAGGGAGGGCTTCACGCCACCCACCCCTGGCCTGCCAGCTGGTAG
 TCCATCAGCACAAATGAAGGAGACTGGAGAAGAGGAAGATAACACTGTTGCTCTGTTCAAGCTGTGTCAGC
 TTTCCCTGGGCTCCAGGACCTCCCTACCTCCACCAACCAAGGGATTATAGCAAAGGCTAACGCT
 AGTTACTCTGGGGTTAGGGAGCCAAAGGCTTAAATAGTTAAGTAGGTGATGGGAAGAGTGGAGATTACCTCA
 TTTAGGGCTCAGGCAGACTCACCTCACATACTCCCTGCTCCCTGTGGTAGAGACACCTGAGAGAGAAAGGGAGGG
 TCAACAATGAGAGAGACCAGGAGTAGGTCTATCAGTGCCCTCAGACTAGAGAGCAATAAGAGGCCAGCCAGTGC
 AGTCCCGGCTGTGTTCTACCTGGTGTAGAAGTGTCTGGTTGCTGGCTGCCATTGCTCTTGACTGG
 GCAGCCCTGGCTGGGCCCCCTCCCTCCGGCCCTCAGTGTGGCTGCTGAGAACGCTCTGGGCTTCCCAAGTGC
 CACGGAGGGTAGGGCTGCTGCTCCATTCTGTACTGGGGGCTGGCTAGGACCTGGGCTGTGGCC
 TCTCAGGGGGCAGCCTCTCCATGGCAGGCATCCCTGCCTGGGCTGCCCTCCCCAGACCCCTGACCACCCCTG
 GGTCTGTCCCCCACCGAGGCCAGGCCAGGCCATCACGGTGTGCTGAGCAGTCCATAGCGCT
 TCTCAATGTGTGTCACCCCGAACCTGGAGGGAGGGAAACACTGGGGTTAGGACCACAAACTCAGAGGCTGCTTG
 GCCCTCCCTCTGACCAAGGGACATCTGAGTTGGTAGCTACTTCCCTCTGGCCTAAGGTAGGGAGGCCCTC
 AGATTGTGGGCACATTGTGAGCTGACTTCTGCTGGAGCTCCAGTCCAGGAGGAAAGAGCCAAGGCCACTT
 TTGGGATCAGGTGCCTGATCACTGGCCCCCTACCTCAGCCCCCTTCCCTGGAGCAGCTGCCCAACTG
 CAGAGAACACAGTGGCTCCCCCTGCGGGGGCGCTTTTCCCTGGAGCAGCTGCCCTGACGGACAAGTGGAG
 GCCTCTGCTGCGGCTGCAATGGATGCAAGGGGCTGCAAGGCCAGGTGACTGTGTGATGATGGGAGGGGCTC
 CGTCCTGAGGCTGGAGGTGGCATCCACACTGGACAGCAGGAGGGAGGGAGTGGAGGTAACATTCCATT
 TCATGTTTGTCTTCTACGTTCTCAGCATGCTCTTAAACCCAGAACGCCCAATTCCCCAAGGCCATT
 TTTCTGTCTTATCTAATAACTCAATATTAAG

FIGURE 178

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401
><subunit 1 of 1, 370 aa, 1 stop
><MW: 40685, pi: 4.53, NX(S/T): 0
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QVSQVKGAARLALLQGAGLDVERWLKPAMTQAQDEVEQERRLSEARLSQRDLSPTAEDAELS
DFEECEETGELFEEPAPQALATRALPCPAHVVFRYQAGREDELTITEGEWLEVIEEGDAEW
VKARNQHGEVGFVPERYLNFPDLSLPESSQDSNPGAEPTAFLAQALYSYTGQSAEELSFP
EGALIRLLPRAQDGVDGFWRGEFGGRGVGVFPSLLVEELLGPPGPELSDPEQMLPSPSPPS
FSPPPAPTSVLDGPPAPVLPGDKALDFPGFLDMMAPRLRPMRPPPPPAKADPGHPDPLT
```

FIGURE 179A

CACAGGGAGACCCACAGACACATATGCACGAGAGAGACAGAGGAGGAAGAGACAGAGACAAAGGCACAGCGGAA
 GAAGGCAGAGACAGGGCAGGCACAGAACAGCGGCCAGACAGACTCCTACAGAGGGAGAGGCCAGAGAAGCTGCAGA
 AGACACAGGCAGGGAGAGACAAAGATCCAGGAAAGGAGGGCTCAGGAGGAGTTGGAGAAGCCAGACCCCTGG
 GCACCTCTCCAAGCCCAGGACTAAGTTCTCCATTCTTAACGGTCTCAGCCCTCTGAAAACCTTGCC
 TCTGACCTTGGCAGGAGTCAAGCCCCCAGGACTACAGAGAGGAGCTTCAAAGCTAGGGTGTGGAGGACTTGG
 GCCCTAGACGGCCTCAGTCCCTCCAGTCAGTACCGTGCAGTACCGTGC**ATG**TCCCAGCAGGCTCGCATCCCGGAGGG
 CTTGGCAGGGCCTGGCTGTGGGAGCCCAACCCCTGCCCTCTGCCAGGAGGAGCTTCCAGGCTGTGGCTGGTGTG
 GCTGCTCTGCTACTGCTGGCTCTCCTGCCCTCAGCCGGCTGGCCAGGCCCCCTCCCCGGGAGGAGGAGAT
 CGTGTTCAGAGAACGCTCAACGGCAGCGTCTGCCCTGGCTGGGCGCCCTGCCAGGCTGTGTGCCGCTTGCA
 GCCCTTGGGAGACGCTGCTACTAGAGCTGGAGCAGGACTCCGGTGTGCAGGAGGGCTGACAGTGCAGTA
 CCTGGGCCAGGCCTGAGCTGGGTGGAGCAGAGCTGGCACCTACCTGACTGGCACCATCAATGGAGATCC
 GGAGTCGGTGGCATCTGCACTGGATGGGGAGCCCTGTTAGGGTGTACAATATGGGGGCTGAACTCCA
 CCTCCAGCCCCCTGGAGGGAGGCACCCCTAACACTGCTGGGGACCTGGGCTCACATCCTACGCCGAAGAGTCC
 TGCCAGCGGTCAAGGTCCATGTGCAACGTCAAGGCTCTTGGAGCAGGCCCCAGCCCCAGACCCGAAGAGCCAA
 GCGCTTGCTTCACTGAGTAGATTGGAGACACTGGTGGTGGAGATGACAAGATGGCCGATTCCACGGTGC
 GGGCTAAAGCCTACCTGCTAACAGTGATGGCAGCAGCAGCCAGGCTTCAAGCACCCAGCATCCGCAATCC
 TGTCACTGGTGTGGTGAETCGGCTAGTGATCTGGCTCAGGCAGGAGGGCCCAAGTGGGGCCAGTGCTGC
 CCAGACCCCTGCGCAGCTCTGTGCTGGCAGGGGGCTAACACCCCTGAGGACTGGGCCCTGACCACCTTG
 CACAGCCATTCTGTTACCCGTAGGACCTGTGTGGAGTCTCCACTTGCACAGCTGGGTATGGCTGATGTGG
 CACCGTCTGTGACCCGGCTGGAGCTGTGCCATTGTGGAGGATGATGGCTCCAGTCAGCCTTCACTGCTGCTCA
 TGAACGGGTATGCTCTAACATGCTCCATGACAACCTCAAGCCATGCATCAGTTGAATGGGCTTGTGAGCAC
 CTCTGCCATGTCTGGCCCTGTGATGGCTCATGTGGATCCTGAGGAGGCCCTGGTCCCCCTGCAGTCCCCGCTT
 CATCACTGACTTCTGGACAATGGCTATGGCACTGTCTTAGACAACACCAGAGGCTCCATTGCATCTGCCGT
 GACTTCCCTGGCAAGGACTATGATGCTGACCGCACTGCCAGCTGACCTCGGGCCGACTCACGCCATTGTCC
 ACAGCTGCCGCCCTGTGCTGCCCTGTGGTGTCTGCCACCTCAATGCCATGCCATGTGCCAGACCAAAACA
 CTCGCCCTGGGCCATGGCACACCCCTGCCGGGCGCACAGGCCCTGATGGGCTGCTGCCCTCACATGGACCA
 GCTCCAGGACTTCAATATTCCACAGGCTGGTGGCTGGGCTCTGGGACATGGGTGACTGCTCTGGACCTG
 TGGGGTGGTGTCCAGTTCTCTCCGAGACTGCACGAGGCTGTCCCCGGAAATGGTGGCAAGTACTGTGAGGG
 CCGCCGTACCGCTTCCGCTCTGCAACACTGAGGACTGCCAACCTGGCTCAGCCCTGACCTCCGCCAGGAGCA
 GTGTGCTGCCATCACACCCACCGCACCTCTCAAGAGCTTCCCAAGGCCATGGACTGGGTTCTCGCTACAC
 AGGCGTGGCCCCCAGGACCACTGCAAACACTCACCTGCCAGGCCGGACTGGCTACTACTATGTGCTGGAGCC
 ACGGGTGGTAGATGGACCCCTGTTCCCCGGACAGCTCTCGGTGTGTGCCAGGGCGATGCATCATGCTGG
 CTGTGATCGCATCATTGGCTCCAAGAAGAAGTTGACAAGTGATGGTGTGCCAGGGAGGGACGGTTCTGGTGCAG
 CAAGCAGTCAGGCTCCTCAGGAATTCAAGGTACGGATAACAACAATGTGGTCACTATCCCCGCCGGGGCACCC
 CATTCTGTCCGGCAGCAGGGAAACCCCTGCCACCGGAGCATCTACTTGGCCCTGAAGCTGCCAGATGGCTCCTA
 TGCCCTCAATGGTGAATACACGCTGATGCCCTCCCCACAGATGTGGTACTGCCCTGGGAGTCAGCTTGCCTA
 CAGCGGGGCACTGCAGGCTCAGAGACACTGTCAGGCCATGGCCACTGGCCAGCCTTGAACACTGCAAGTCC
 AGTGGCTGGCAACCCCCAGGACACAGCCTCCGATACAGCTTCTCGTGCCCCGGCCACCCCTCAAGGCCACG
 CCCACTCCCCAGGACTGGCTGCACCGAAGAGCACAGATCTGGAGATCCTTCCGGCGGCCCTGGCGGGCAG
 GAAAT**AA**CCTCACTATCCGGCTGCCCTTCTGGGACCCGGCTCGGACTTAGCTGGAGAAAGAGAGAGCTT
 CTGGTGTGCCCTCATGCTAACAGACTCAGTGGGAGGGCTGTGGGCGTGAGACCTGCCCTCTCTGCCCTAAT
 GCGCAGGCTGCCCTGCCCTGGTTCTGCCCTGGGAGGAGCAGTGATGGTTAGTGGATGAAAGGGGCTGACAGAC
 AGCCCTCCATCTAAACTGCCCCCTGCGGTCAGGGACTACAGGAGGGAGGGGAAAGGCCAGGGAGGGCTGGGCC
 CAGTTGTATTATTAGTATTCACTTTATTAGCACCAGGGAAAGGGGAAACAGGACTAGGGTCTGGTCTGGGAA
 CCTGACCCCTGACCCCTCATAGCCCTCACCTGGGCTAGGAATCAGGGTGTGTGATAGGTATAAGGGT
 TGTGTATGCGTGTGTGTGAAATGTGTGTGTTAGTGTGTTAGGTGAGGACTACACCTGTTCTGCTTCTC
 TTCTGAATTATTTATTTTGGAAAAGAAAAGTCAGGGTAGGGCTGCCCTCAGGGAGTGGAGGATTATCTTT
 TTTTTTTCTTCTTCTTCTTTCTTTCTTTGAGACAGAATCTCGCTCTGTGCCAGGCTGGAGTGAATGCAATG
 GCACAATCTCGGCTCACTGCATCCTCCGCCCTCCGGGTTCAAGTGTGATTCTCATGCCCTCAGCCTCTGAGTAGCTG
 GGATTACAGGGCTCCTGCCACCACGCCAGCTAATTGTTGTTGTTGTTGGAGACAGAGTCTCGCTATTGTC
 ACCAGGGCTGGAATGATTCACTGCAACCTTCGCCACCTGGGCTCAGCAATTCTCTGCCCTAGCCTCC
 CGAGTAGCTGAGATTAGGCACCTACCACCAAGGCCGGCTAATTGTTGATTTTAGTAGAGACAGGGTTTCAC
 CATGTTGGCCAGGCTGGCTCGAACCTCTGACCTTAGGTGATCCACTGCCCTCATCTCCAAAGTGTGGGATT
 ACAGGGCTGAGGCCACCGTGCCTGGCCACGCCAACTAATTGTTGATTTTAGTAGAGACAGGGTTTACCATGT
 TGGCCAGGCTGCTCTGAACTCCTGACCTCAGTAATGACCTGCCCTCCCAAAGTGTGGGATTACAGG
 TGTGAGGCCACACGCCGGTACATATTTAAATTGAATTCTACTATTGATGATCCTTGGAGTCAGACAG

FIGURE 179B

ATGTGGTTGCATCCTAACTCCATGTCCTGAGCATTAGATTCTCATTTGCCAATAATAACCTCCCTTAGAAG
TTTGTGTGAGGATTAATAATGTAATAAGAACTAGCATAACACTCAAAAAAAAAAAAAAAAAGGAAA
AAAAAAAAAAAAAAAAAAAAAAAAGGAAA

FIGURE 180

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492
><subunit 1 of 1, 837 aa, 1 stop
><MW: 90167, pi: 8.39, NX(S/T): 1
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FPEKLNGSVLPGSGAPARLLCRLQAFGETLLELEQDSGVQVEGLTVQYLGQAPELLGGAEP
GYLTGTINGDPESVASLHWGGALLGVLQYRGAELHLQPLEGGTPNSAGGPGAHILRRKSP
ASGQGPMCNVKAPLGSPSPRRAKRFAASLSRFVETLVVADDKMAAFHGAGLKRYLLTVMAA
AAKAKFKHPSIRNPVSLVVTRLVILGSGEEGPVQGPSAQTLRSFCAWQRGLNTPEDSGPDHF
DTAILFTRQDLCGVSTCDTILGMADVGTVCDCPARSCAIVEDDGLQSAFTAHELGHVFNMLHD
NSKPCISLNGPLSTSRRHVMAPVMAHVDPPEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHL
PTVFPGKDYDADRCQLTFGPDSRHCPCQLPPPACAALWCSGHLNGHAMCQTKHSPWADGTPCG
PAQACMGGRCLHMDQLQDFNIPQAGGWGPWGDCSRTCGGGVQFSSRDCTRPRVPRNGGKY
CEGRRTRFRSCNTEDCPTGSALTFREEQCAAYNHRTDLFKSFPGPMWDWPRTGVAPQDQCK
LTCQARALGYYVLEPRVVDGTPCSPDSSSVCVQGRCIHAGCDRIIGSKKKFDKCMVCGGDG
SGCSKQSGSFRKFRYGYNNVVTIPAGATHILVRQQGNPGHRSIYLALKLPDGSYALNGEYTL
MPSPTDVVLPGAVSLRYSGATAASETLSGHGPLAQPLTLQVLVAGNPQDTRLRYFFVPRPT
PSTPRPTPQDWLHRRAQILEILRRRWAGRK
```

Important features of the protein:

Signal peptide:

amino acids 1-48

N-glycosylation site.

amino acids 68-71

Glycosaminoglycan attachment site

amino acids 188-191, 772-775

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 182-185

Tyrosine kinase phosphorylation site.

amino acids 730-736

N-myristoylation sites.

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-582, 679-684, 682-687, 763-768

Amidation sites.

amino acids 560-563, 834-837

Leucine zipper pattern.

amino acids 17-38, 24-45

Neutral zinc metallopeptidases, zinc-binding region signature.

amino acids 358-367

FIGURE 181

CAGCAGTGGTCTCTCAGCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACC**ATGG**
CAAAGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTAAATCC
AAGAAAATATGTAATCACTTAAGATTTGTGGACTGGTGTGTTGGTATCCTGGCCCTAACTCT
AATTGTCCTGTTGGGGAGCAAGCACCTCTGGCCGGAGGTACCCAAAAAGCCTATGACA
TGGAGCACACTTCTACAGCAATGGAGAGAAGAAGAAGATTTACATGGAAATTGATCCTGTG
ACCAGAACTGAAATATTAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTT
AAAAAACGGATAACACTGGCATCTACTTCGTGGTCTTCAAAATGTTTATCAAAACTCAGA
TTAAAGTATTGATTCTGAATTCTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACC
ACAACTTCTTGAAACAGTCAGTGATTGGTCCCAGCAGAAAGCCTATTGAAAACCGAGA
TTTCTTAAAAATTCCAAAATTCTGGAGATTGTGATAACGTGACCATGTATTGGATCAATC
CCACTCTAATATCAGTTCTGAGTTACAAGACTTGAGGAGGGAGAAGATCTTCACTTT
CCTGCCAACGAAAAAAAAGGGATTGAACAAAATGAACAGTGGTGGTCCCTCAAGTGAAAGT
AGAGAAGACCGTCACGCCAGACAAGCAAGTGAGGAAGAACTTCCAATAATGACTATACTG
AAAATGGAATAGAATTGATCCCAGCTGGATGAGAGAGGTTATTGTTGATTACTGCCGT
CGAGGCAACCGCTATTGCCGCCGCTGTGAACCTTACTAGGCTACTACCCATATCCATA
CTGCTACCAAGGAGGACGAGTCATCTGTCGTGTCATCATGCCCTGTAACTGGTGGTGGCCC
GCATGCTGGGAGGGTC**TAA**AGGAGGTTGAGCTCAAATGCTAAACTGCTGGCAACATAT
AATAATGCATGCTATTCAATGAATTCTGCCTATGAGGCATCTGGCCCTGGTAGCCAGCT
CTCCAGAATTACTGTAGGTAATTCTCTCTCATGTTCTAATAAAACTTCTACATTATCACC
AAAAAAAAAAAAAAAAAA

FIGURE 182

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73727
><subunit 1 of 1, 317 aa, 1 stop
><MW: 37130, pi: 5.18, NX(S/T): 3
MAKNPPENCEDCHILNAEAFSKKICKSLKICGLVFGILALTЛИLFWGSKHFWPEVPKKAY
DMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKT
QIKVIPEFSEPEEEIDENEETTTFFEQSVIWWPAEKPIENRDFLKNKILEICDNVTMYWI
NPTLISVSELQDFEEEGEDLHF PANNEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDY
TENGIEFDPMMLDERGYCCIYCRRGNRYCRRVCEPLLGGYPYPYCYQGGRVICRVIMPCNWWV
ARMLGRV
```

Important features of the protein:

Signal peptide:

amino acids 1-40

Transmembrane domain:

amino acids 25-47 (type II)

N-glycosylation sites.

amino acids 94-97, 180-183

Glycosaminoglycan attachment sites.

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

N-myristoylation sites.

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

Microbodies C-terminal targeting signal.

amino acids 315-317

Cytochrome c family heme-binding site signature.

amino acids 9-14

FIGURE 183

GCGGAACCTGGCTCCGGCTGGCACCTGAGGAGCGGCGTGACCCCGAGGGCCCAGGGAGCTGCC
 CGGCTGGCCTAGGCAGGCAGCCGACCA**ATG**GCCAGCACGGCGTGAGCTTCTGGGCTTCCT
 GCTCAGCTCCTGGGCATGGTGGGCACGTTGATCACCACCATCCTGCCGACTGGCGGAGGA
 CAGCGCACGTGGGCACCAACATCCTCACGGCGTGTCTACCTGAAAGGGCTCTGGATGGAG
 TGTGTGTGGCACAGCACAGGCATCTACCAAGTGCAGATCTACCGATCCCTGCTGGCGCTGCC
 CCAAGACCTCCAGGCTGCCCGGCCCTCATGGTCATCTCCTGCCCTGCCATAGCCT
 GCGCCTGCCCGTCATGGGATGAAGTGCACCGCGTGCACGGCAAGGGCACACCCGCAAGACC
 ACCTTGCCATCCTCGGCGCACCCCTTCATCCTGCCGCCCTGTGCATGGTGGCGT
 CTCCCTGGACCAACGACGTGGTGCAGAACTTCTACAACCCGCTGCTGCCAGGGCATGA
 AGTTTGAGATTGCCAGGCCCTGTACCTGGGTTCATCTCCTCGTCCCTCGCTCATTGGT
 GCCACCCCTGCTTGCCCTGCCAGGACGAGGCACCCCTACAGGCCCTACCAGGGCCCCGCC
 CAGGGCCACCAACGACCACTGCAAACACCGCACCTGCCTACCAGCCACCAGCTGCCACAAAG
 ACAATGGGCCCCCTCAGTGACCTCGGCCACGCACAGCGGTACAGGCTGAACGACTACGTG
TGAGTCCCCACAGCCTGTTCTCCCTGGCTGCTGTGGCTGGTCCCCGGCGGGACTGTC
 AATGGAGGCAGGGGTTCCAGCACAAAGTTACTTCTGGCAATTTGTATCCAAGGAAATA
 ATGTGAATGCGAGGAAATGTCTTAGAGCACAGGGACAGAGGGGAAATAAGAGGAGGAGAA
 AGCTCTATACCAAAGACTGAAAAAAAATCCTGTCTGTTTGATTTATTATATATAT
 TTATGTGGGTGATTGATAACAAGTTAATATAAGTGACTTGGGAGTTGGTCAGTGGGGT
 TGTTTGTGATCCAGGAATAAACCTGCGGATGTGGCTGTTATGAAAAAAA

FIGURE 184

MASTAVQLLGFLLSFLGMVGTLITTIPLPHWRRTAHVGTNILTAVSYLKGLWMECVWHSTGIY
QCQIYRSLLALPQDLQAARALMVISCLLSGIACACAVIGMKCTRCAKGTPAKTTFAILGGTL
FILAGLLCMVAWSWTNDVVQNFYNPLLPSGMKFEIGQALYLGFISSSLSLIGGTLLCLSCQ
DEAPYR PYQAPPRATT TANTAPAYQPPAAYKDNRAPS VTSATHSGYRLNDYV

Important features of the protein:

Signal peptide:

amino acids 1-21

Transmembrane domains:

amino acids 82-103, 115-141, 160-182

FIGURE 185

GAGCTCCCTCAGGAGCGCGTTAGCTCACACCTCGGCAGCAGGAGGGCGGCAGCTTCTCG
 CAGGCAGGGCGGGCGGCCAGGATC**ATG**TCCACCACATGCCAAGTGGTGGCGTTCCT
 CCTGTCCATCCTGGGCTGGCGCTGCATCGCGCCACCGGGATGGACATGTGGAGCACCC
 AGGACCTGTACGACAACCCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGC
 GTGAGGCAGAGTTCAGGCTCACCGAACATGCAGGCCATTTCACCATCCTGGACTTCAGC
 CATGCTGCAGGCAGTGCAGGCCATTGATGATCGTAGGCATCGTCTGGTGCCATTGGCTCC
 TGGTATCCATCTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAGGC
 AACATGACACTGACCTCCGGATCATGTTATTGTCTCAGGTCTTGCAATTGCTGGAGT
 GTCTGTGTTGCCAACATGCTGGTACTAACTTCTGGATGTCCACAGCTAACATGTACACCG
 GCATGGGTGGATGGTGCAGACTGTTCAGACCAGGTACACATTGGTGCGGCTCTGTTCTG
 GGCTGGTCGCTGGAGGCCTCACACTAATTGGGGTGTGATGATGTGCATGCCCTGCCGGGG
 CCTGGCACCAAGAACCAACTACAAAGCCTTCTTATCATGCCCTAGGCCACAGTGGT
 CCTACAAGCCTGGAGGCTCAAGGCCAGCACTGGCTTGGTCCAACACCAAAAACAAGAAG
 ATATACGATGGAGGTGCCGCACAGAGGACGAGGTACAATCTTATCCTCCAAGCACGACTA
 TGTG**TAAT**GCTCTAACGACCTCTCAGCACGGCGGAAGAAACTCCGGAGAGCTACCCAAAA
 AACAAAGGAGATCCCCTAGATTCTTCTTGCTTTGACTCACAGCTGAAAGTTAGAAAAGC
 CTCGATTTCATCTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTGTCTCAAATATTCC
 ACCATAAAACAGCTGAGTTATTGAATTAGAGGCTATAGCTCACATTTCATCCTCTAT
 TTCTTTTTAAATATAACTTCTACTCTGATGAGAGAATGTGGTTAATCTCTCTCAC
 ATTTGATGATTAGACAGACTCCCCCTTCCCTCAGTCAATAAACCCATTGATGATCTA
 TTTCCCAGCTTATCCCCAAGAAAACCTTGAAAGGAAAGAGTAGACCCAAAGATGTTATT
 CTGCTGTTGAATTGTCTCCCCACCCCCAACTTGGCTAGTAATAAACACTTACTGAAGAA
 GAAGCAATAAGAGAAAGATATTGTAATCTCTCCAGGCCATGATCTCGGTTTCTACACTG
 TGATCTAAAGTTACCAACCAAAGTCATTTCAGTTGAGGCAACCAAACCTTCTACTG
 CTGTTGACATCTCTTATTACAGCAACACCATTCTAGGAGTTCTGAGCTCTCCACTGGAG
 TCCTCTTCTGCGGGTCAGAAATTGCCCTAGATGAATGAGAAAATTATTTTTAAAT
 TTAAGTCCTAAATATAGTTAAAATAAATAATGTTTAGTAAAATGATAACTATCTCTGTGA
 AAATAGCCTCACCCCTACATGTGGATAGAAGGAAATGAAAAATAATTGCTTGACATTGTCT
 ATATGGTACTTGTAAAGTCATGCTTAAGTACAAATTCCATGAAAAGCTCACACCTGTAATC
 CTAGCACTTGGGAGGCTGAGGAGGAAGGATCACTTGAGGCCAGAAGTTCGAGACTAGCCTG
 GGCAACATGGAGAAGCCCTGTCTCACAAATACAGAGAGAAAAATCAGCCAGTCATGGTG
 GCATACACCTGTAGTCCAGCATTCCGGAGGCTGAGGTGGGAGGATCACTTGAGCCCAGGG
 AGGTTGGGCTGCAGTGAGCCATGATCACACCACTGCACTCCAGCCAGGTGACATAGCGAGA
 TCCTGTCTAAAAAAATAAATAATGGAACACAGCAAGTCCTAGGAAGTAGGTTAAA
 ACTAATTCTTAA

FIGURE 186

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734
><subunit 1 of 1, 261 aa, 1 stop
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MSTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLWRSCVRQSSGFTE
CRPYFTILGLPAMILQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIM
FIVSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTL
IGGVMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFCASTGFGSNTKNKKIYDGGARTE
DEVQSYP SKHDYV
```

Signal peptide:

amino acids 1-23

Transmembrane domains:

amino acids 81-100, 121-141, 173-194

FIGURE 187

GGAAAAACTGTTCTTCTGTGGCACAGAGAACCTGCTCAAAGCAGAAGTAGCAGTTCCG
 GAGTCCAGCTGGCTAAACTCATCCCAGAGGATA**ATGGCAACCCATGCCTTAGAAATCGCTG**
 GGCTGTTCTGGTGGTGGAAATGGTGGCACAGTGGCTGTCAGTGTGATGCCTCAGTGG
 AGAGTGTGGCCTTCATTGAAAACACATCGTGGTTTGAAAACCTCTGGGAAGGACTGTG
 GATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGG
 CTCTTCTCCGGACCTACAGGCAGCCAGAGGACTGATGTGCTGCTCCGTGATGTCCTTC
 TTGGCTTCATGATGCCATCCTGGCATGAAATGCACCAGGTGCACGGGGACAATGAGAA
 GGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTCATCACGGCATGGTGGTGC
 TCATCCCTGTGAGCTGGGTTGCCAATGCCATCATCAGAGATTCTATAACTCAATAGTAAT
 GTGCCCAAAACGTGAGCTGGAGAAGCTCTACTTAGGATGGACCACGGCACTGGTGC
 GATTGTTGGAGGAGCTCTGCTGCGTTTGCAACGAAAAGAGCAGTAGCTACA
 GATACTCGATACTTCCCATCGCACACCCAAAAAGTTATCACACCGAAAGTCACCG
 AGCGTCACTCCAGAAGTCAGTATGTG**TAG**TGTATGTTTAACTTTACTATAAGC
 CATGCAAATGACAAAAATCTATATTACTTTCTAAAATGGACCCAAAGAAACTTGATTAA
 CTGTTCTTAACTGCCTAATCTTAATTACAGGAACTGTGCATCAGCTATTATGATTCTATAA
 GCTATTCAGCAGAATGAGATATTAAACCCAATGCTTGATTGTTCTAGAAAGTATAGTAAT
 TTGTTTCTAAGGTGGTCAAGCATCTACTCTTTATCATTACTTCAAAATGACATTGCT
 AAAGACTGCATTATTTACTACTGTAATTCTCCACGACATAGCATTATGTACATAGATGAG
 TGTAACATTATCTCACATAGAGACATGCTTATGGTTATTAAAATGAAATGCCAG
 TCCATTACACTGAATAATAGAACTCAACTATTGCTTTCAGGGAAATCATGGATAGGGTTG
 AAGAAGGTTACTATTAATTGTTAAAACAGCTTAGGGATTAATGTCCTCCATTATAATGA
 AGATTAAAATGAAGGTTAATCAGCATTGTAAGGAAATTGAATGGCTTCTGATATGCTG
 TTTTTAGCCTAGGAGTTAGAAATCCTAACTCTTATCCTCTCTCCCAGAGGCTTTTT
 TTCTTGTGTTAAATTAAACATTAAAACGCAGATATTGTCAGGGCTTGCATTCA
 AACTGCTTCCAGGGCTACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGTG
 GTTTAGGAAAGTGAAAATATTTGTTTGTATTGAAGAAGAATGATGCATTGACAA
 GAAATCATATGTATGGATATATTAAATAAGTATTGAGTACAGACTTGAGGTTCATC
 AATATAAAATAAGAGCAGAAAAATATGTCTGGTTTCACTGCTTACCAAAAAACAAACA
 ACAAAAAAAAGTTGTCCTTGAGAACTTCACCTGCTCCTATGTGGGTACCTGAGTC
 AAAATTGTCATTGTTCTGTGAAAATAAAATTCCCTCTGTACCATTCTGTTAGTTACTAA
 ATCTGTAAATACTGTATTCTGTTATTCCAATTGATGAAAAGTACAATCCAATTG
 AAGTTGTCGACGTCTGTCTAGCTAAATGAATGTGTTCTATTGCTTACACATTATA
 TTAATAAAATTGTACATTCTAATT

100
 99
 98
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 96
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 21
 20
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 10
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 6
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 4
 3
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FIGURE 188

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MATHALEIAGLFLGGVGMVGTVAVTVMPQWRVSAFIENNIVFENFWEGLWMNCVRQANIRM
QCKIYDSLLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRGTGDNEKVKAHILLTAGI
IFIITGMVVLIPVSWANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVF
CCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV
```

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 82-101, 118-145, 164-188

FIGURE 189

TCGCC**ATG**CCTCTGCCGGAATGCAGATCCTGGGAGTCGTCTGACACTGCTGGGCTGGGTG
 AATGGCCTGGTCTCCTGTGCCCTGCCCATGTGGAAAGGTGACCGCTTCATCGGAAACAGCAT
 CGTGGTGGCCCAGGTGGTGGGAGGGCCTGTGGATGTCCTGCGTGGTGCAGAGCACCGGCC
 AGATGCAGTGCAAGGTGTACGACTCACTGCTGGCGCTGCCACAGGACCTGCAGGCTGCACGT
 GCCCTCTGTGTCATGCCCTCCTGTGGCCCTGTTGGCTGCTGGTCTACCTGCTGGGC
 CAAGTGTACCACCTGTGTGGAGGAGAAGGATTCCAAGGCCGCCTGGTGCACCTCTGGGA
 TTGTCTTGTCATCTCAGGGCTGACGCTAATCCCCGTGTGGACGGCGCATGCCATC
 ATCCGGGACTTCTATAACCCCTGGTGGCTGAGGCCAAAAGCGGGAGCTGGGGCCTCCCT
 CTACTTGGCTGGCGGCCTCAGGCCCTTGTGCTGGTGGGGTTGCTGTGCCTGCACCT
 GCCCCTCGGGGGGGTCCCAGGGCCCCAGCCATTACATGCCCGCTACTAACATCTGCCCT
 GCCATCTCTCGGGGCCCTGAGTACCCCTACCAAGAATTACGT**TGA**CGTGGAGGGAAATG
 GGGGCTCCGCTGGCGTAGAGCCATCCAGAAGTGGCAGTGCCAACAGCTTGGATGGTT
 CGTACCTTTGTTCTGCCTGCTATTTCTTTGACTGAGGATATTAAAATTCAATT
 GAAAACTGAGCCAAGGTGTTGACTCAGACTCTCACTTAGGCTCTGCTGTTCTACCCCTGG
 ATGATGGAGCAAAGAGGGATGCTTGAGATTCTGGATCTGACATGCCCATTTAGAAGC
 CAGTCAAGCTATGGAACATGGAGGCTGCTGCTGGCTTCCCTAGATGTCACTGGACAGCTG
 TGCCCCAAGAGTTCTGCTGCTGGGGCTGGCTTCCCTAGATGTCACTGGACAGCTG
 CCCCCCATCCTACTCAGGTCTCTGGAGCTCCCTCTTCACCCCTGGAAAAACAAATCATCTG
 TTAACAAAGGACTGCCACCTCCGGAACCTGACCTGTTCTCCGCTGATAAGACG
 TCCACCCCCCAGGCCAGGTCCCAGCTATGTAGACCCCCGCCACCTCAAACACTGCACC
 CTTCTGCCCTGCCCTCGTCTCACCCCTTACACTCACATTATCAAATAAGCATG
 TTTGTTAGTGCA

FIGURE 190

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73736
><subunit 1 of 1, 220 aa, 1 stop
><MW: 23292, pi: 8.43, NX(S/T): 0
MASAGMQILGVVLTLGLGVNGLVSCALPMWKVTAFIGNSIVVAQVVWEGLWMSCVVQSTGQM
QCKVYDSLLALPQDLQAARALCVIALLVALFGLLVYLAGAKCTTCVEEKDSKARLVLTSGIV
FVISGVTLIIPVCWTAHAIIRDFYNPLVAEAQKRELGASLYLGWAASGLLLGGGLLCCTCP
SGGSQGPSPHYMARYSTSAPAIISRGPSEYPTKNYV
```

Transmembrane domains:

amino acids 8-30 (type II), 82-102, 121-140, 166-186

FIGURE 191

GCCAAGGAGAACATCATCAAAGACTTCTAGACTCAAAAGGCTTCCACGTTCTACATCTTG
AGCATCTTCTACCACCTCCGAATTGAACCAGTCTCAAAGTAAAGGCAATGGCATTATCCC
TTGCAAATTGCTGGCTGGTCTTGGGTCCTGGCATGGTGGGACTCTGCCACAACCC
TCTGCCTCAGTGGTGGAGTATCAGCTTGTTGGCAGAACATTATTGTCTTGAGAGGGCTC
TGGGAAGGGCTCTGG**ATG**AATTGCATCCGACAAGCCAGGGTCCGGTTGCAATGCAAGTTCTA
TAGCTCCTTGTGGCTCTCCGCCTGCCCTGGAAACAGCCCAGGCCCTCATGTGTGGCTG
TTGCTCTCCTTGATGCCCTGCTTATTGGCATCTGGCATGAAGCAGGTCCAGTGCACA
GGCTCTAACGAGAGGGCAAAGCATACCTCTGGAACTTCAGGAGTCCTCATCCTGAC
GGGTATCTCGTTCTGATTCCGGTGAGCTGGACAGCCAATATAATCATCAGAGATTCTACA
ACCCAGCCATCCACATAGGTAGAAACGAGAGCTGGAGCAGCACTTTCTGGCTGGCA
AGCGCTGCTGTCCTCTTCATTGGAGGGGTCTGCTTGTGGATTGCTGCTGCAACAGAAA
GAAGCAAGGGTACAGATATCCAGTGCCCTGGCTACCGTGTGCCACACACAGATAAGCGAAGAA
ATACGACAATGCTTAGTAAGACCTCCACCAAGTTATGTC**TAA**TGCCCTCTTGGCTCCAAGT
ATGGACTATGGTCAATGTTTTATAAAGTCCTGCTAGAAACTGTAAGTATGTGAGGCAGGA
GAACCTGCTTATGTCTAGATTACATTGATACGAAAGTTCAATTGTTACTGGTGGTAGG
AATGAAAATGACTTACTGGACATTGACTTCAGGTGTATTAAATGCATTGACTATTGTTG
GACCCAATCGCTGCTCCAATTCATATTCTAAATTCAAGTATAACCCATAATCATTAGCAAG
TGTACAATGATGGACTACTTATTACCTTTGACCATCATGTATTATCTGATAAGAATCTAAA
GTTGAAATTGATATTCTATAACAATAAAACATATACCTATTCTA

FIGURE 192

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73737
><subunit 1 of 1, 173 aa, 1 stop
><MW: 18938, PI: 9.99, NX(S/T): 1
MNCIRQARVRLQCKFYSSLLALPPALETARALMCVAVALSLIALLIGICGMKQVQCTGSNER
AKAYLLGTSGVLFILTGIFVLIPIVSWTANIIIRDYNPAlHIGQKRELGAALFLGWASAAVL
FIGGGLLCGFCCCNRKKQGYRYPVPGYRVPHTDKRRNTMLSKTTSYV
```

Important features of the protein:

Transmembrane domains:

amino acids 31-51, 71-90, 112-133

N-glycosylation site.

amino acids 161-164

FIGURE 193

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTCCAGC**ATG**AAGATCACTGGGGT
CTCCTTCTGCTCTGTACAGTGGTCTATTCTGTAGCAGCTCAGAAGCTGCTAGTCAGTCTCC
AAAAAAAGTGGACTGCAGCATTACAAGAAGTATCCAGTGGTGGCCATCCCCTGCCCATCA
CATACCTACCAGTTGTGGTCTGACTACATCACCTATGGGAATGAATGTCACTTGTGTACC
GAGAGCTGAAAAGTAATGGAAGAGTTCAGTTCTCACGATGGAAGTTGC**TAA**ATTCTCCA
TGGACATAGAGAGAAAGGAATGATATTCTCATCATCTTCATCATCCCAGGCTCTGACTG
AGTTTCTTCAGTTTACTGATGTTCTGGGTGGGGACAGAGCCAGATTCAAGTAATCTTG
ACTGAATGGAGAAAGTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCAGCAT
TTTTTTTTAACACGTCAATAAAAAATAATCTCCCAGA

FIGURE 194

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73739
><subunit 1 of 1, 85 aa, 1 stop
><MW: 9232, pI: 7.94, NX(S/T): 0
MKITGGLLLLCTVYYFCSSSEAASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGN
ECHLCTESLKSNDRVQFLHDGSC
```

Signal peptide:

amino acids 1-19

FIGURE 195

CCCGCGCCCGGTTCTCCCTCGCAGCACCTCGAAGTGC~~GCCCCTGCCCTCCTGCTCGCGCCC~~
~~CGCCGCC~~**ATG**GCTGCCCTCCCCCGCGGGCTGCTGTCCTGGCCCTGACCGGGCTGGCGCTGC
TCCTGCTCCTGTGCTGGGCCAGGTGGCATAAGTGGAAATAACTCAAGCTGATGCTCAA
AAACGAGAACGACCTGTTCCA~~ACTAAGACTAAAGTGGCCGTTGATGAGAATAAAGCCAAAGA~~
ATT~~CCTTG~~GCAGCCTGAAGCGCCAGAAC~~GCAGCTGTGGGACCGACTCGGCCGAGGTGC~~
AGCAGTGGTACCAGCAGTTCTACAT~~GGGCTTGATGAAGCGAAATTGAAGATGACATC~~
ACCTATTGGCTTAACAGAGAT~~CGAAATGGACATGAATACTATGGCGATTACTACCAACGTCA~~
CTATGATGAAGACTCTGCAATTGGT~~CCCGGAGCCCTACGGCTTAGGCATGGAGCCAGCG~~
TCAACTACGATGACTAC**TAA**CCATGACTGCCACACGCTGTACAAGAAGCAAATAGCGATT~~C~~
TCTTCATGTATCTCCTAATGCCTACACTACTGGTTCTGATTGCTCTATTCAGCAGAT
CTTTCTACCTACTTGTGATCAAAAAAGAAGAGTTAAAACAACACATGTAAATGCCTT
TGATATTCATGGGAATGCCTCTCATTTAAAAATAGAAATAAAGCATTGTTAAAAGA

FIGURE 196

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742
><subunit 1 of 1, 148 aa, 1 stop
><MW: 17183, PI: 8.77, NX(S/T): 0
MAASPARPAVLALTGLALLLLLWGPGGISGNKLKLMQKREAPVPTKTKAVDENAKEFL
GSLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNDRNGHEYGDYYQRHYD
EDSAIGPRSPYGYFRHGASVNYDDY
```

Signal peptide:

amino acids 1-30

FIGURE 197

CGGCTCGAGCCGCCGGAAAGTGCCCGAGGGGCCGCGATGGAGCTGGGGAGCCGGCGCTC
 GGTAGCGCGCGGGCAAGGCAGGCGCC**ATG**ACCTGATTGAAGGGTGGGTATGAGGTGAC
 CGTCCTTTCTCGGTGCTTGCTGCCTGCCTCTGGTCTGCCCTGCCCTGGTCTAACGCACA
 CCGCTGAGGGCGGGGACCCACTGCCAGCCGTAGGGACCCAACGCCATCCCAGCCCAGC
 GCAGCCATGGCAGCTACCGACAGCATGAGAGGGAGGCCAGGGCAGAGACCCCCAGCCT
 GAGACACAGAGGTCAAGCTGCACAGCCAGAGCCAGCACGGGTTCACAGAACACCGCCAG
 CCCCGGACTCCCCGAGGAGCCCTCGTGCTACGGCTGAAATTCCCTAATGATTAGCAGAGCAG
 GTGGCCAGGGCCTGGCCCCACGACACCATTGGCTCCTTGAAAAGGACCCAGTTCCGGCCG
 GGAAACAGCAGGTGCGACTCATCTACCAAGGGCAGCTGCTAGGCGACGACACCCAGACCCCTGG
 GCAGCCTTCACCTCCCTCCAACTGCCTCTCCACTGCCACGTGTCCACGAGAGTCGGTCCC
 CCAAATCCCCCTGCCCGCCGGGTCCGAGCCCGCCCTCCGGCTGGAAATGGCAGCCT
 GCTGCTGCCCTGCTGCTCCTGCTGTTGCTGCTGCTCTGGTACTGCCAGATCCAGTACCGGC
 CCTTCTTCCCTGACCGCCACTCTGGCCTGCCGGCTTCACCTGCTCCTCAGTCTCCTG
 GCCTTGCCATGTACCGCCCG**TAG**GCCTCCGCCGGCGTTGGCAGCGTCGCCGGCCCTCC
 GGACCTTGCTCCCCGCGCCGCCGGAGCTGCTGCCCTGCCAGGCCGCTCTCCGGCCTG
 CCTCTTCCCGCTGCCCTGGAGCCCAGCCCTGCCCGCAGAGGACTCCGGACTGGCGGAGG
 CCCCGCCCTGCGACCGCCGGGCTCGGGGCCACCTCCGGGCTGCTGAACCTCAGCCGCA
 CTGGGAGTGGCTCCTCGGGCTCGGGCATCTGCTGTCGCTGCCCTGGCCCCGGCAGAGCCG
 GGCGCCCCGGGGCCGTCTAGTGTGCTGCCGGAGGACCCAGCCGCTCCAATCCCTGAC
 AGCTCCTTGGCTGAGTTGGGACGCCAGGTCGGTGGAGGCTGGTAAGGGAGCGGGAG
 GGGCAGAGGAGTTCCCCGGAACCCGTGCAGATTAAAGTAAGTGTGAAGTTAAAAAAAAA
 AAAAAAAA

FIGURE 198

MTLIEVGVDVTVLFSVLACLLVLALAWVSTHTAEGGDPLPQPSGTPTPSQPSAAMAATDSM
RGEAPGAETPSLRHRGQAAQPEPSTGFTATPPAPDSPQEPLVRLKFLNDSEQVARAWPHDT
IGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRVGPPNPPCPPGS
EPGPSGLEIGSLLLPLLLLLLWYCQIQYRPFFPLTATLGLAGFTLLSLLAFAMYRP

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 195-217

FIGURE 199

GAGATTGGAAACAGCCAGGTTGGAGCAGTGAGTGAGTAAGGAAACCTGGCTGCCCTCTCCAG
ATTCCCCAGGCTCTCAGAGAAGATCAGCAGAAAGTCTGCAAGACCCTAACGAAACCACATCAGCCC
TCAGCTGCACCTCCTCCCTCCAAGG**ATG**ACAAAGGCCTACTCATCTATTGGTCAGCAGC
TTTCTTGCCCTAAATCAGGCCAGCCTCATCAGTCGCTGTGACTTGGCCCAGGTGCTGCAGC
GGAGGACTTGGATGGTTGAGGGTTACTCCCTGAGTGACTGGCTGTGCCTGGCTTTGTGG
AAAGCAAGTTAACATATCAAAGATAAAATGAAAATGCGGATGGAAGCTTGACTATGGCCTC
TTCCAGATCAACAGCCACTACTGGTGCAACGATTATAAGAGTTACTCGGAAAACCTTGCCA
CGTAGACTGTCAAGATCTGCTGAATCCAACCTTCTGCAGGCATCCACTGCGAAAAAGGA
TTGTGTCCGGAGCACGGGGATGAACAACTGGGTAGAATGGAGGTTGCAGTGTTCAGGCCGG
CCACTCTCCTACTGGCTGACAGGATGCCGCTGAGA**TGA**AACAGGGTGCGGGTGCACCGTGG
AGTCATTCCAAGACTCCTGTCCTCACTCAGGGATTCTCATTCTTCTTCCACTGCCTCCA
CTTCATGTTATTTCTCCCTCCATTACAACAAAATGACCAGAGCCCCAGGAATAAA
TGGTTTCTGGCTCCTCCTACTCCCCTGACCCAGTCCCCTGGTTCTGTCTGTTAT
TTGTAAACTGAGGACCACAATAAGAAATCTTATATTATCG

FIGURE 200

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746
><subunit 1 of 1, 148 aa, 1 stop
><MW: 16896, pI: 6.05, NX(S/T): 1
MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGYSLSDWLCLAFVESKFNISKI
NENADGSFDYGLFQINSHYWCNDYKSYSSENLCVDCQDLLNPNILLAGIHCAKRIVGARGMN
NWVEWRLHCSGRPLSYWLTGCRLR
```

Signal peptide:

amino acids 1-18

FIGURE 201

TCTGACCTGACTGGAAGCGTCCAAAGAGGGACGGCTGTCA~~G~~CCCTGCTT~~G~~ACTGAGAACCCA
 CCAGCTCATCCCAGACACCTCATAGCAACCTATTATACAAAGGGGAAAGAAACACCTGAG
 CAGAATGGAATCATTTTTCCCAAGGAGAAAACC~~G~~GGTAAAGGGAGGGAAAGCAATTCA
 AATTGAAAGTCCCTGTGAATGGGCTT~~C~~AAGGCAATTAAAGAAATCCACTCAGAGAGGAC
 TTGGGGT~~G~~AAACTGGGTCTGTGGTTCTGATTGTAAGT~~G~~GAAGCAGGTCTGCACACGC
 TGTTGGCAAATGTCAGGACCAGGTTAAGTGACTGGCAGAAAAACTCCAGGT~~G~~GAACAAGCA
 ACCCATGTTCTGCTGCAAGCTTAGCAAC**ATG**CTCTAAGGAAGCGATA~~C~~AGGCACAGACC~~A~~T
 CTGTTGCATTGGCAAGTTCTAGCAAC**ATG**CTCTAAGGAAGCGATA~~C~~AGGCACAGACC~~A~~T
 CAGACTCCAGTCCCTGCTGCTCCTGATGCTGGGATGCGTCTGATGATGGTGGCGATGT
 TGCACCCCTCCCCACCACACCC~~T~~GCACCAGACTGT~~C~~ACAGCCAAGCCAGCAAGCACAGCCCT
 GAAGCCAGGTACCGCCTGGACTTGGGAATCCCAGGATTGGGTACT~~G~~GAAGCTGAGGATGA
 GGGTGAAGAGTACAGCCCTGGAGGGC~~T~~GCCACCCTTATCTCACT~~G~~CGGGAGGATCAGC
 TGCTGGTGGCCGTGGC~~T~~ACCCCCAGGCCAGAAGGAACCAGAGCCAGGGCAGGAGAGGTGGG
 AGCTACCGCCTCATCAAGCAGCCAAGGAGG~~C~~AGGATAAGGAAGCCCCAAAGAGGGACTGGG
 GGCTGATGAGGACGGGAGGTGTGAAGAAGAGGAGT~~G~~ACCCGTT~~C~~AGCCTGGACCCAC
 GTGGCCTCCAGGAGGC~~A~~CTCAGT~~G~~CCCGCATCCCCCTCAGAGGGCT~~T~~GCCCGAGGT~~G~~CG
 CACCCACTGTGT~~C~~GCAGCAGCACCC~~T~~CAGGACAGCCTGCCACAGCCAGCGT~~C~~ATCCTCTG
 TTTCCATGATGAGG~~C~~CTGGTCCACTCTCCTGCGGACTGT~~A~~CACAGCATCCTCGACACAGT~~G~~C
 CCAGGGCCTCCTGAAGGAGATCATCCTCGT~~G~~ACGACCTCAGCAGCAAGGACA~~A~~CTCAAG
 TCTGCTCTCAG~~G~~AA~~T~~ATGTGGCCAGGCTGGAGGGG~~T~~GAAGTTACTCAGGAGCAACAAGAG
 GCTGGGTGCCATCAGGGCCCG~~A~~TGCTGGGGCCACCAGAGCCACCGGG~~A~~TGTGCTCGTCT
 TCATGGATGCCACT~~G~~CAGT~~G~~CCACCAGGCTGGT~~G~~AGGCC~~T~~CTCAGCAGAA~~T~~AGCT
 GGTGACAGGAGGCC~~G~~AGTGGT~~A~~TAGATGTGATTGACT~~G~~GAAGACTTTCCAGTA
 TTACCCCTCAAAGGAC~~T~~GCAGCGTGGG~~T~~GTTGGACT~~G~~GAAGCTGGATTCCACTGGGAAC
 CTTGCCAGAGCATGTGAGGAAGGCC~~T~~CCAGT~~C~~CCCCATAAGCCC~~A~~T~~C~~AGGAGCC~~T~~GTG
 GTGCCCGGAGAGGTGGTGGCCATGGACAGACATTACTCCAAA~~A~~CTGGAGCGT~~A~~TGACTC
 TCTTATGTCGCT~~G~~CGAGGTGGT~~G~~AAA~~A~~CTCGA~~A~~CTGT~~C~~TTCAAGGC~~T~~GGCT~~T~~GTGGT~~G~~
 GCTCTGTTGAA~~A~~TCCTCC~~T~~GCTCTCGGGTAGGACACATCTACCAAA~~A~~CTCAGGATTCC~~C~~AT
 TCCCCCCTCGACCAGGAGGCC~~A~~CC~~T~~GAGGAACAGGG~~T~~CGCAT~~G~~T~~G~~AGAC~~T~~GGCT~~G~~GG
 GTCATTCAAAGAAACCTTCTACAAGCATAGCCCAGAGGC~~T~~CTCCTTGAGCAAGGCTGAGA
 AGCCAGACTGCAT~~G~~GAACG~~T~~GCAGCTGCAAAGGAGACTGGG~~T~~GT~~G~~CGACATTCCACTGG
 TTTCTGGCTAATGTCTACCC~~T~~GAGCTGTACCC~~A~~T~~T~~GAACCCAGGCCAGTTCTCTGGAAA
 GCTCCACAA~~A~~CTGGACTTGGC~~T~~CTGTGCAGACTGCCAGGCAGAAGGG~~A~~CATCCTGGG~~C~~T
 GTCCC~~A~~TGGTGGCTCT~~T~~GCAGTGACAGCCGGCAGCAACAGTACCTGCAGCACACCAGC
 AGGAAGGAGATT~~C~~ACT~~T~~GGCAGGCCACAGCACCTGTGCT~~T~~GT~~C~~AGGCAGGAGCAGGT
 GATTCTTCAGAA~~C~~GT~~G~~ACGGAGGAAGGCC~~T~~GGC~~A~~TC~~C~~ACCAGCAGCACTGGACTCCAGG
 AGAATGGG~~A~~TGATTGTCCACATTCTTCTGGAAATGCAT~~G~~GAAGCTGTGGT~~G~~CAAGAAAAC
 AATAAAGATTGTACCT~~G~~CGTCC~~G~~TGT~~G~~ATGGAAAAGGCCGCCAGCAGTGGCGATTGACCA
 GATAAA~~T~~GCTGTGGATGAACGA**TGA**ATGTCAATGT~~C~~AGAAGAAAAGAGAATT~~T~~TGGCCATC
 AAAATCCAGCTCCAAGTGAACGTAAAGAGCTTATATATT~~C~~ATGAAGCTGATCCTTTGTGT
 GTGTGCTCCTTGTGTAGGAGAGAAAAAGCTATGAAGAATATAGGAAG~~T~~TTCTCCTT
 TCACACCTTATT~~C~~ATTGACTGCTGGCTGCTTA

FIGURE 202

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760
><subunit 1 of 1, 639 aa, 1 stop
><MW: 73063, pI: 6.84, NX(S/T): 2
MLLRKRYRHRPCRLQFLLLLLMLGCVLMVMVAMLHPPHHTLHQTVTAQASKHSPEARYRLDFG
ESQDWVLEAEDEGEEYSPLEGLPPFISLREDQLLVAVALPQARRNQSQGRRGGSYRLIKQPR
RQDKEAPKRDWGADEDGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHP
QDSLPTASVILCFHDEAWSTLLRTVHSILDTPRAFLKEIILVDDLSQQGQLKSALSEYVAR
LEGVKLLRSNKRLGAIRARMLGATRATGDVLVFMDAHCECHPGWLEPLLSRIAGDRSRVVSP
VIDVIDWKTFQYYPSKDLQRGVLDWKLDFHWEPLPEHVRKALQSPISPIRSPVVPGEVVAMD
RHYFQNTGAYDSLMSLRGGENLELSFKAWLCGGSVEILPCSRVGHIFYQNQDSHSPLDQEATL
RNRVRIAETWLGSFKETFYKHSPEAFSLSKAEKPDCMERLQLQRLGCRTFWFLANVPEL
YPSEPRPSFSGKLHNTGLGLCADCQAEGDILGCPVLAPCSDSRQQQYLQHTSRKEIHFGSP
QHLCFAVRQEQQVILQNCTEEGLAIHQHQHWDFOENGIVHILSGKCMEAVVQENNKDLYLRPC
DGKARQQWRFQINAVDER
```

Signal peptide:

amino acids 1-28

FIGURE 203

CGCCAAGCATGCAGTAAAGGCTGAAAATCTGGGTACAGCTGAGGAAGACCTCAGAC**ATGGA**
 GTCCAGGATGTGGCTGCGCTGCTGCTGCCACCTCCTCCCTCTGGCCACTGCTGTTGC
 TGCCCCCTCCCACCGCCTGCTCAGGGCTTCTCATCCTCCCTCGAACCCCCACCAGCCCCAGCC
 CGCCCCCCCCTGTGCCAGGGAGGCCCTCGGCCACGTCATGTGTGCGTGTGGAGCGAGC
 ACCTCCACCAAGCCGATCTCCTCGGGTCCAAGATCACGTCGGCAAGTCCTGCCTGGCACTG
 CACCCCCAGCCACCCATCAGGCTTGAGGAGGGGCCCTCATCCAAATACCCCTGGGCT
 ATCGTGTGGGTCCCACCGTGTCTCGAGAGGATGGAGGGGACCCAACTCTGCCAATCCCAG
 ATTCTGGACTATGGTTTGAGCCCTCATGGGCTCGAACCCCCACACCCAACTCAGACT
 CCATGCGAGGTGATGGAGATGGGTTATCCTGGAGAGGCACCTGCCACCCCTGCCGATT
 CTGTTGGGGGCCGTGGGAAGGTGTGGACCCCCAGCTCTATGTCACAATTACCATCTCCAT
 CATCATTGTTCTCGGCCACTGGCATCATCTCAAGTTCTGCTGGGACCGCAGCCAGAAGC
 GACGCAGACCCCTCAGGGCAGCAAGGTGCCCTGAGGCAGGAGGAGGCCAGCAGCCACTGACA
 GACCTGTCCCCGGCTGGAGTCACTGTGCTGGGGCCTCGGGGACTCACCTACCCCCACCC
 TGACCATGAGGAGGCCGAGGGGACCCCGCTGGGATGCCCAACCCAAAGGGGCTCCAG
 CCTTCCAGTTGAACCGG**TGAGGGCAGGGCAATGGGATGGGAGGGCAAAGAGGGAAAGGAAAC**
 TTAGGTCTTCAGAGCTGGGTGGGGTGCCTCTGGATGGTAGGTAGTGAGGAGGCAGGCAGTGGC
 CTCCCACAGCCCCCTGGCCCTCCAAAGGGGCTGGACAGCTCCTCTGGGAGGCACCCCTTC
 CTTCTCCAGTCTCAGGATCTGTGCTATTCTGCTGCCATAACTCCAACTCTGCC
 TCTTGTTTTCTCATGCCACCTGTCTAAAGACAACCTGCCCTTTAACCTTGATTCCC
 CCTCTTGCTTGAACCTCCCTCTATTCTGCCCTACCCCTTGTTCTGACTGTGCCCTT
 TCCCTCTCCCTCTCAGGATCCCCCTGGTAATCTGTGATGCCCAATGTTGGGGTGCAGCC
 AAGCAGGAGGCCAAGGGGCCGGCACAGCCCCCATCCACTGAGGGTGGGGCAGCTGTGGGGA
 GCTGGGCCACAGGGCTCCTGGCTCTGCCCTTGACACCACCCGGAACACTCCCCAGCC
 CCACGGCAATCCTATCTGCTGCCCTCCTGCAGGTGGGGCCTCACATATCTGTGACTTCG
 GGTCCCTGTCCCCACCCCTGTGCACTCACATGAAAGCCTTGACACTCACCTCCACCTCAC
 AGGCCATTGACACGCTCTGCACCCCTCTCCCCGTCCATACCGCTCCAGCTGACTCT
 CATGTTCTCTCGTCTCACATTGCACTCTCTCTTCCACATTCTGTGCTCAGCTCACTCAG
 TGGTCAGCGTTCTGCACACTTACCTCTCATGTGCTTCCCGCCTGATGTTGGTGG
 TGTGCGGCGTGTCACTCTCCCTCATGAACACCCACCCACCTCGTTCCGCAGCCCTGC
 GTGCTGCTCAGAGGTGGGGAGGTGAGCTGGGGCCTTGCCCTCATCGGTGATGG
 TCTCGTCCCATTCCACACCATTGTTCTGTCTCCCCATCCTACTCCAAGGATGCCGGCA
 TCACCCCTGAGGGCTCCCCCTGGGAATGGGGTAGTGAGGCCAGACTTCACCCCCAGGCCA
 CTGCTAAATCTGTTCTGACAGATGGGTTTGGGAGTCGCCTGCTGCACTACATGAGAA
 AGGGACTCCCATTGCCCTCCCTTCTCCTACAGTCCCTTGTCTGCTGCTGCTGGCTG
 TCTGTGTGTGCCATTCTCTGGACTTCAGAGCCCCCTGAGCCAGTCCTCCCTCCAGCCT
 CCCCTGGCCCTCCCTAACCTCCACCTAGGCTGCCAGGGACCGGAGTCAGCTGGTTCAAGGCC
 ATCGGGAGCTCTGCCCTCAAGTCTACCCCTCCCTCCGGACTCCCTCTGTCCCCCTCTT
 CCTCCCTCTCCACTCTCCTCTTGTCTCCCTGCCCTTCCCCCTCTCAGGTT
 CCTCCCTCTCTCACTGGTTTCCACCTTCCCTTCCCTTCCCTGGCTCTAGGCT
 GTGATATATATTTGTATTATCTCTTCTTGTGGTGTGATCATTTGAATTACTGTG
 GGATGTAAGTTCAAAATTCAAATAAGCCTTGCAAGATAA

FIGURE 204

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393
><subunit 1 of 1, 243 aa, 1 stop
><MW: 26266, pI: 8.43, NX(S/T): 1
MRPQGPAAASPQRRLGLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGV
PGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA
ECTFTKMRNSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGPLPIEAIYLDQGSPEMN
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIEELPK
```

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

FIGURE 205

GTAAACCAGCGCAGTCCTCCGTGCGTCCC GCCGCTGCCCTCACTCCGGCCAGG**ATGG**
CATCCTGTCTGGCCCTGCGCATGGCGCTGCTGGTCTCCGGGTTCTGGCCCTGCGGTG
CTCACAGACGATGTTCCACAGGAGCCC GTGCCACGCTGTGGAACGAGCCGGCGAGCTGCC
GTCGGGAGAAGGCCCCGTGGAGAGCACCAGCCCCGGCCGGAGGCCGTGGACACCGGTCCCC
CAGCCCCCACC GTCGCGCCAGGACCCGAGGACAGCACCGCGCAGGAGCGGCTGGACCAGGGC
GGCGGGTCGCTGGGCCCGGCCTATCGCGGCCATCGT GATCGCCGCCCTGCTGGCCACCTG
CGTGGTGCTGGCGCTCGTGGTCGT CGCCTGAGAAAGTTTCTGCCTCC**TGA**AGCGAATAAA
GGGGCCGCCCGGCCGCGACTCGGCAAAAAAAAAAAAAAA

FIGURE 206

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398
><subunit 1 of 1, 121 aa, 1 stop
><MW: 12073, pI: 4.11, NX(S/T): 0
MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPVESTSPGREPVDTG
PPAPTVAPGPEDSTAQERLDQGGGSLPGAIAAIVIAALLATCVVLALVVVALRKFSAS
```

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 91-110

Glycosaminoglycan attachment site.

amino acids 44-47

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 116-119

N-myristylation site.

amino acids 91-96

FIGURE 207

GGCGTGGTGGTGGCGCGCTGAAGGGTGTGGCGCAGCAGCGTCGGTGGTGGCCGGCG
 CGGGCCGGGACGGGC**ATG**GCCCTGCTGCTGCCTGGTGTGCCTGACGGCGGCGTGGCCA
 CGGCTGTCTGCACTGCCACAGCAACTTCTCCAAGAAGTTCTCCTTCTACCGCCACCATGTGA
 ACTTCAAGTCCTGGTGGGTGGCGACATCCCCGTGTCAGGGCGCTGCTCACCGACTGGAGC
 GACGACACGATGAAGGAGCTGCACCTGGCCATCCCCGCAAGATCACCCGGAGAAGCTGGA
 CCAAGTGGCGACAGCAGTGTACCAGATGATGGATCAGCTGTACCAGGGAAAGATGTACTTCC
 CCGGGTATTCCCCAACGAGCTGCAAACATCTCCGGGAGCAGGTGCACCTCATCCAGAAC
 GCCATCATCGAAAGGCACCTGGCACCAGGCAGCTGGGAGGAGGGCAGCTCTCAGGGAGGG
 ACCCAGCCTAGCACCTGAAGGATCAATGCCATCACCCCGGGGACCTCCCC**TAA**GTAGCCC
 CCAGAGGCGCTGGGAGTGTGCCACCGCCCTCCCTGAAGTTGCTCCATCTCACGCTGGGG
 GTCAACCTGGGGACCCCTCCCTCCGGGCCATGGACACACATACTGAAAACCAGGCCGCAT
 CGACTGTAGCACCGCTGTGGCATCTCCAGTACGAGACCATCTCTGCAACAACTGCACAG
 ACTCGCACGTCGCCTGCTTGCTATAACTGCGAGTAGGGCTCAGGCATCACACCCACCGT
 GCCAGGGCCCTACTGTCCCTGGGTCCAGGCTCTCCTGGAGGGGGCTCCCCGCCTCCAC
 CTGGCTGTCACTGGGTAGGGCGGGCGTGGGTTAGGGCGCACCCTCAAGCCTGTGT
 CCCACAGGTCTCGCGCAGTGGAAAGTCAGCTGTCCAGGGCTCCTGAACACTACATAAAAC
 TGGCACAAAGTAAGTCCCCTCCTCAAACCAACACAGGCAGTGTGTATGTGAGCACCTCGT
 GGTGAGTATGTGTGGGCACAGGCTGGCTCCCTCAGCTCCCACGTCTAGAGGGCTCCC
 GGAGGTGGAACCTCAACCCAGCTCTGCGCAGGAGGCGGCTGCAGTCCTTCTCCCTCAAAG
 GTCTCCGACCCCTCAGCTGGAGGCAGGCTTAAAGGGCTCCATAGGGTCTGGTCC
 ACCCATCCCAGGTCTGTGGTCAGAGCCTGGAGGGTCCCTACGATGGTTAGGGTGC
 ATGGAGGGCTGACTGCCACATTGCCTTCAGACAGGACACGAGCATGAGGTAAGGCC
 CCTGACCTGGACTTCAGGGGAGGGGTAAGGGAGAGAGGGAGGGGGCTAGGGGCTCT
 AGATCAGTGGGGCACTGCAGGTGGGCTCTCCCTACCTGGACACCTGCTGGATGTAC
 CTCTGCAACCACACCCATGTGGTGGTTCATGAACAGACGCTCTGCCTCTCCTGG
 CCTGGACACACAGAGCCACCCGGCCTGTGAGTGACCCAGAGAAGGGAGGCCTGGAGA
 AGGGTGCTCGTAAGCCAACACCAGCGTGCAGGCGCTGCACACCCCTGGACATCCCAGGC
 ACGAGGGTGTGATGTGGCACACATAGGACCACACGTCCAGCTGGAGGGAGGGCCT
 GGGGCCCCCAGGGAGGGAGGCAGGGGTGGGGACATGGAGAGAGCTGAGGCAGC
 CCTGGCAGCCTGGTATGCCAGCCTTAAGGTGTCTGGAGCCCCACACTTGGCAACCTGAC
 TGGAAGATGCTGCTGAGTGTCTCAAGCAGCAGTACGAGCAGCTGGCCTGCCCCAGGG
 GTGGGGGGGGAGACTCAGCTGGACAGCCCTGCCTGTCACTCTGGAGCTGGCTGCTGC
 CTCAGGACCCCTCTCGACCCGGACAGAGCTGAGCTGGCAGGGCAGGAGGGCGGGAGG
 GAGGGAAATGGGGTGGCTGTGCGCAGCATCAGCGCCTGGCAGGTCCGAGAGCTGC
 TGTGATTAAAGTCCCTGATTTCTC

FIGURE 208

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399
><subunit 1 of 1, 157 aa, 1 stop
><MW: 17681, pI: 7.65, NX(S/T): 1
MALLLCLVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSWWVGDI
PVSGALLTDWSDDTMK
ELHLAIPAKITREKLDQVATAVYQMMMDQLYQGKMYFPGYFPNELRNIFREQVHLIQN
AIIER
HLAPGSWGGQLSREGPSLAPEGSMPSPRGDLP
```

Signal peptide:

amino acids 1-15

FIGURE 209

AGCAGGAGCAGGAGAGGGACA**ATG**GAAGCTGCCCGTCCAGGTCATGTTCTCTTATTCT
 CCTCACGTGTGAGCTGGCTGCAGAAGTTGCTGCAGAAGTTGAGAAATCCTCAGATGGTCCTG
 GTGCTGCCAGGAACCCACGTGGCTCACAGATGTCCCAGCTGCCATGGAATTCAATTGCTGCC
 ACTGAGGTGGCTGTCATAGGCTTCTCCAGGATTAGAAAATACCAGCAGTGCCCCACTCCA
 TAGCATGGTGCAAAAATTCCCAGGCAGTCATTGGGATCAGCACTGATTCTGAGGTTCTGA
 CACACTACAACATCACTGGAACACCCTGCCTCTTCGCCTGGTAGACAATGAACAACTG
 AATTAGAGGACGAAGACATTGAAAGCATTGATGCCACCAAATTGAGCCGTTTCAATTGAGAT
 CAACAGCCTCCACATGGTGACAGAGTACAACCCGTGACTGTGATTGGGTTATTCAACAGCG
 TAATTCAATTGATTCATCTCCTCTGATAATGAACAAAGGCCTCCCCAGAGTATGAAGAGAACATG
 CACAGATACCAGAAGGCAGCCAAGCTCTCCAGGGGAAGATTCTCTTATTCTGGTGGACAG
 TGGTATGAAAGAAAATGGGAAGGTGATATCATTTCAAACTAAAGGAGTCTCAACTGCCAG
 CTTGGCAATTACCACTAGATGACGAGTGGATACACTGCCACAGCAGAACAGTTCC
 GTAGAGCATGTGCAAAACTTTGTGATGGATTCTAAGTGGAAAATTGTTGAAAGAAAATCG
 TGAATCAGAAGGAAAGACTCCAAAGGTGGAAC**TGA**CTTCTCCTGGAACTACATATGCC
 AAGTATCTACTTATGCAAAGTAAAAGGCACAACACTCAAATCTCAGAGACACTAAACAAACAG
 GATCACTAGGCCTGCCAACACACACACACACAGCTCATTCTGTCTAAATCTGTTTC
 ACACACGCGCACACACACACACACAGAGCTCATTCTGTCTAAATCTGTTTC
 TTCTCCTCTTTAAATTTCATATCCTCACTCCCTATCCAATTCTCTTATCGTGCATT
 CATACTCTGTAAGCCCACATCTGTAACACACACTAGATCAAGGCTTAAGAGACTCACTGTGATG
 CCTCTATGAAAGAGAGGCATTCTAGAGAAAGATTGTTCAATTGTCATTAAATATCAAGT
 TTGTATACTGCACATGACTTACACACACATAGTTCTGCTTTAAGGTTACCTAAGGGT
 TGAAACTCTACCTTCTTCATAAGCACATGTCCGTCTGACTCAGGATCAAAACCAAAGG
 ATGGTTTAAACACCTTGTGAAATTGTCTTTGCCAGAAGTTAAAGGCTGTCTCCAAGTC
 CCTGAACTCAGCAGAAATAGACCATGTGAAAACCTCCATGCTGGTTAGCATCTCCAACCTCCC
 TATGTAATCAACAAACCTGCATAATAAATAAAAGGCAATCATGTTATA

FIGURE 210

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401
><subunit 1 of 1, 273 aa, 1 stop
><MW: 30480, pI: 4.60, NX(S/T): 1
MEAAPSRFMFLFLLTCELAAEVAEEVKSSDGPAGAAQEPWTLDVPAAMEFIAATEVAVIG
FFQDLEIPAVPILHSMVQKFPGVSGISTDSEVLTHYNITGNTICLFRDVDNEQLNLEDEDI
ESIDATKLSRFIEINSLHMVTEYNPVTIVIGLFNSVIQIHLLIMNKASPEYEENMHRYQKAA
KLFQGKILFILVDGMKENGKVISFFKLKESQLPALAIYQTLDEWDTLPTAEVSVEHVQNF
CDGFLSGKLLKENRESEGKTPKVEL
```

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 143-162

FIGURE 211

GGAGAGCCGCGGCTGGACCGGAGTGGGAGCGCGCGTGGAGGTGCCACCCGGCGGGGTG
 GCGGAGAGATCAGAAGCCTCTTCCCCAAGCCGAGCCAACCTCAGCGGGGACCCGGGCTCAGG
 GACGCGGCGGCGGCGGCGACTGCAGTGGCTGGACG**ATG**GCAGCGTCCGCCGGAGCCGGG
 GCGGTGATTGCAGCCCCAGACAGCCGGCGCTGGCTGTGGTGGTGGCTGGCGGGCGCTTGG
 GCTCTTGACAGCTGGAGTATCAGCCTGGAAGTATATACGCCAAAAGAAATCTCGTGGCAA
 ATGGTACACAAGGGAAGCTGACCTGCAAGTTCAAGTCTACTAGTACGACTGGCGGGTTGACC
 TCAGTCTCCTGGAGCTCCAGCCAGAGGGGCCGACACTACTGTGTCGTTTCCACTACTC
 CCAAGGGCAAGTGTACCTGGGAATTATCCACCATTAAAGACAGAACATCAGCTGGCTGGAG
 ACCTTGACAAGAAAGATGCATCAATCACATAGAAAATATGCAGTTATACACAATGGCACC
 TATATCTGTGATGTCAAAAACCCCTCCTGACATCGTGTCCAGCCTGGACACATTAGGCTCTA
 TGTCGTAGAAAAAGAGAATTGCCTGTGTTCCAGTTGGTAGTGGTGGGCATAAGTTACTG
 CTGTGGCCTAGGTCTCACTCTGCTCATCAGCATGATTCTGGCTGTCCTCTATAGAAGGAAA
 AACTCTAACGGGATTACACTGGCTGCAGTACATCAGAGAGTTGTCACCAGTTAACAGGC
 TCCTCGGAAGTCCCCCTCCGACACTGAGGGCTTGTAAAGAGTCTGCCTCTGGATCTCACC
 AGGGCCCAGTCATATATGCACAGTTAGACCACCTCCGGCGGACATCACAGTGACAAGATTAAC
 AAGTCAGAGTCTGTGGTGTATCGGGATATCGAAAGAAT**TAA**GAGAACATACCTAGAACATATC
 CTCAGCAAGAAACAAACAAACTGGACTCTCGTCAGAAAATGTAGCCCATTACCACATGT
 AGCCTTGGAGACCCAGGCAAGGACAAGTACACGTGTACTCACAGAGGGAGAGAAAGATGTGT
 ACAAAAGGATATGTATAAATATTCTATTAGTCATCCTGATATGAGGAGGCCAGTGTGCATGA
 TGAAAAGATGGTATGATTCTACATATGTACCCATTGTCTGCTGTTTGTACTTCTTTTC
 AGGTCATTACAATTGGGAGATTCAGAAACATTCTTACCATCATTAGAAATGGTTG
 CCTTAATGGAGACAATAGCAGATCCTGTAGTATTCCAGTAGACATGGCCTTTAATCTAAG
 GGCTTAAGACTGATTAGTCTTAGCATTACTGTAGTTGGAGGATGGAGATGCTATGATGGAA
 GCATACCCAGGGTGGCCTTTAGCACAGTATCAGTACCAATTATTGTCTGCCGCTTTAAAAA
 AATACCCATTGGCTATGCCACTGAAAACAATTGAGAAGTTTTGAAGTTTTCTCACT
 AAAATATGGGCAATTGTTAGCCTACATGTTGTGTAGACTTACCTAAGTTGCACCCCTG
 AAATGTGTATCAATTCTGGATTATAAGCAAGATTAGCAAAGGATAATGCCGAAG
 GTCACTTCATTCTGGACACAGTTGGATCAAACTGATTAAGTAGAAAATCCAAGCTTGCTT
 GAGAACTTTGTAACGTGGAGAGTAAAAAGTATCGGTTTA

FIGURE 212

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76510
><subunit 1 of 1, 269 aa, 1 stop
><MW: 29082, pI: 9.02, NX(S/T): 3
MAASAGAGAVIAAPDSRRWLWSVLAAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKFKS
TSTTGGLTSVSWSFQPEGADTTVSFFHYSQGQVYLGNYPPFKDRISWAGDLDKKDASINEN
MQFIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVVVGIVTAVVLGLTLLISM
LAVLYRRKNSKRDYTGCSTSESLSPVKQAPRKSPSDTEGLVKSLPSGSHQGPVIYAQLDHSG
GHHSOKINKSESVVYADIRKN
```

Signal peptide:

amino acids 1-37

Transmembrane domain:

amino acids 161-183

FIGURE 213

GCCGGCTGTGCAGAGACGCC**ATG**TACCGGCTCCTGTCAGCAGTGACTGCCGGCTGCCGCC
 CCCGGGGCTTGGCCTCAAGCTCGGGACGACGCCGGTCCATCAGCGCGCCGGCTGCCGCC
 TCTCGGCCACGGCTGGTCGGGGCCTCGGGCTGGGCTGGGCTGGCGCTGGGGTGAAGC
 TGGCAGGTGGGCTGAGGGCGCCGGCCCCGGCGCAGTCCCCCGCGCCCCGACCTGAGGCG
 TCGCCTCTGGCGAGCCGCCACAGGAGCAGTCCTCGCCCCGTGGTCTCCGAGACCCGGC
 GCCGCCCTGCTCCAGGTGCTCGCCAGAGCCATCGAGAGCAGCCGACCTGCTGCACAGGA
 TCAAGGATGAGGTGGCGCACCGGCATAGTGGTTGGAGTTCTGTAGATGGAAAAGAAGTC
 TGGTCAGAAAGTTAGGTTATGCTGATGTTGAGAACCGTGTACCATGTAAACCAGAGACAGT
 TATGCGAATTGCTAGCATCAGCAAAAGTCTCACCATGGTTGCTCTGCCAAATTGTGGAAAG
 CAGGGAAACTGGATCTTGATATTCCAGTACAACATTATGTTCCGAATTCCCAGAAAAAGAA
 TATGAAGGTGAAAAGGTTCTGTACACAACAAGATTACTGATTTCCCATTAAAGTGGAAATTG
 TCATTATGAAAAGGACATAAAAAGGTGAAAGAAGAGAAAGCTTATAAAGCCTTGAAGATGA
 TGAAAGAGAATGTTGCATTGAGCAAGAAAAAGAAGGCAAAAGTAATGAAAAGAATGATTT
 ACTAAATTAAAACAGAGCAGGAGAATGAAGCCAATGCCGAATTCAAAACCTGGCAAGAA
 AAAGAATGATTTGAACAAGGCGAATTATATTGAGAGAAAAGTTGAAAATTCAATTGAAT
 CCTTAAGATTATTAAAAATGATCCTTGTCTCAAACCTGGTAGTCAGTTGTATTCA
 ACTTTGGCTATACCTACTGGCAGCCATAGTAGAGAGAGCTCAGGATGAAATATTGGA
 CTATATGCAGAAAATATTCCATGACTGGATATGCTGACGACTGTGCAGGAAGAAAACGAGC
 CAGTGATTACAATAGAGCAAGG**TAA**ATGAATACCTCTGCTGTCTAGCTATATCGCATC
 TTAACACTATTTATTAATTAAAAGTCAAATTCTTGTTCATTCCAAATCAACCTGC
 CACATTTGGGAGCTTCTACATGTCTGTTCTCATCTGAAAGTGAAGGAAGTAAAACA
 TGTTATAAAGTAAAAAAA

FIGURE 214

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522
><subunit 1 of 1, 373 aa, 1 stop
><MW: 41221, pI: 8.54, NX(S/T): 0
MYRLLSAVTARAAPGGLASSCGRRGVHQRAGLPPPLGHGWGGLGLGLALGVKLAGGLRG
AAPAQSPAAPDPEASPLAEPHQEQSLAPWSPQTPAPPCSRCAFARAIESSRDLLHRIKDEVGA
PGIVVGVSVDGKEVWSEGLGYADVENRVPCKPETVMRIASISKSLSLTVALAKLWEAGKLDLD
IPVQHYVPEFPEKEYEGERKSVTTRLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAF
EQEKEGKSNEKNDFTFKTEQENEAKCRNSKPGKKNDFEQGELYLREKFENSIESLRLFKN
DPLFFKPGSQFLYSTFGYTLAAIVERASGCKYLDYMQKIFHDLDMLTTVQEENEPVIYNRAR
```

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 39-60

FIGURE 215

GTGACACTATAGAAGAGCTATGACGTGCATGCACCGTACGTAAGCTCGGAATTGGCTCG
 AGGCTGGTGGGAAGAACCGAGA**ATG**CGGGCAGCCAGCGCTGGGCAACCCGGCTGCTCCTGC
 TCTGCTGATGGCGGTAGCAGCGCCAGTCGAGCCCAGGGCAGCGGCTGCCGGCCGGACT
 GGTGCGCAGGGGCTGGGCGGAAGGTCGAGAGGGCGAGGCCTGTGGCACGGTGGGCTGCT
 GCTGGAGCACTCATTGAGATCGATGACAGTGCCAACCTCCGAAGCGGGCTCACTGCTCT
 GGAACCAGCAGGATGGTACCTGTCCCTGTACAGCGCAGCTCAGCGAGGAGGAGCGGGC
 CGACTCCGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGGATCCAAAGGCACCCGG
 GCCCTGGATGGCCTGGAAGCTGGTGGCTATGTCTCCTCCTTGTCCCTGCGTGCTCCCTGG
 TGGAGTCGCACCTGTCGGACCAGCTGACCCCTGCACGTGGATGTGCCGGAACGTGGTGGC
 GTGTCGGTGGTGACGCACCCGGGGCTGCCGGGCCATGAGGTGGAGGACGTGGACCTGGA
 GCTGTTAACACCTCGGTGCAGCTGCAGCCGCCACCACAGCCCCAGGCCCTGAGACGGCGG
 CCTCATTGAGCGCCTGGAGATGGAACAGGCCAGAAGCCAAGAACCCCCAGGAGCAGAAG
 TCCTTCTCGCAAATACTGGATGTACATCATTCCGTCCTGTTCTCATGATGTCAGG
 AGGCCAGACACCGGGGCCAGGGTGGGGTGGGGTGGGGTAGTGGCC
 TTTGCTGTGCCACCCCTCCCTG**TAA**GTCTATTAAAAACATCGACGATACTGAAATGTG
 TGAACGTTTGAAAAGCTACAGCTCCAGCAGCCAAAGCAACTGTTGGCAAGACGG
 TCCTGATGTACAAGCTTGATTGAAATTCACTGCTCACTGATACTGTTATTGAAACCCAAG
 GAATGGCTGTCCCCATCCTCATGTCGGCTGTGGAGCTCAGCTGTGTTGTGGCAGTTAT
 TAAACTGTCCCCAGATCGACACGCAAAAAAAA

FIGURE 216

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76529
><subunit 1 of 1, 269 aa, 1 stop
><MW: 28004, pI: 5.80, NX(S/T): 1
MAAASAGATRLLLLLMAVAAPSRARGSGCRAGTGARGAGAEGREGEACGTVGLLLEHSFEI
DDSANFRKRGSLWNQQDGTLSLSQRQLSEEERGRLRDVAALNGLYRVRIPRPGALDGLEA
GGYVSSFVPACSLVESHLSDQLTLHVDVAGNVVGVSVVTHPGGCRGHEVEDVDLELFNTSVQ
LQPPTTAPGPETAAFIERLEMEQAQAKNPQEOKSFFAKYWMYIIPVVLFLMMMSGAPDTGGQ
GGGGGGGGGGGGSGLCCVPPSL
```

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 226-243

FIGURE 217

GGAGCGCTGCTGGAACCGAGCCGGAGCCGGAGCCACAGCAGGGAGGGTGGCCTGGCGGCCT
 GGAGCCGGACGTGTCGGGGCGTCCCCGAGACCGGGGCAGCAGGTGTCGTCGGGGGCCACC
ATGCTGGTGACTGCCTACCTGCTTTGTAGGCCTCCTGGCCTCCTGCCTGGGCTGGAAC
 GTCAAGATGCCGGCTAAACCCCTGGAAGGGCCTGCAGCAATCCTCCTCCTCGGTTTC
 AACTGGACTTCTATCAGGTCTACTCCTGGCCCTGGCAGCTGATTGGCTTCAGGCCCCCTAC
 CTCTATAAACTCTACCAGCATTACTACTTCCTGGAAGGTCAAATTGCCATCCTCTATGTCTG
 TGGCCTGCCTCTACAGTCCTCTTGGCTAGTGGCCTCCTCCCTGTGGATTGGCTGGTC
 GCAAGAATTCTTGTGTCCTCTCCCTGACTTAACACTATGCTGCTAACCAAACCTCT
 CAAGACTACTTGTGCTGCTAGTGGGGCAGCACTTGGTGGCTGTCCACAGCCCTGCTCTT
 CTCAGCCTTCGAGGCCTGGTATATCCATGAGCACGTGGAACGGCATGACTCCCTGCTGAGT
 GGATCCCAGCTACCTTGCTCGAGCTGCCTCTGGAACCATGTGCTGGCTGTAGTGGCAGGT
 GTGGCAGCTGAGGCTGTAGCCAGCTGGATAGGCTGGGCCTGTAGC GCCCTTGTGGCTGC
 CATCCCTCTCCTGGCTCTGGCAGGGCCTTGGCCCTCGAAACTGGGGGAGAACTATGACC
 GGCAGCGTGCCTCTCAAGGACCTGTGCTGGAGGCCTGCGCTGCCTCCTGTCGGACCGCCGC
 GTGCTGCTGCTGGCACCATACAAGCTCTATTGAGAGTGTATCTCATCTTGCTTCCT
 CTGGACACCTGTGCTGGACCCACACGGGGCCCTCTGGCATTATCTTCTCCAGCTTCAG
 CAGCCAGCCTGCTGGCTCTCCCTGTACCGTATGCCACCTCCAAGAGGTACCACCTTCAG
 CCCATGCACCTGCTGCCCTGCTGTGCTCATCGTGTCTCTCTCATGTTGACTTT
 CTCTACCAGCCCAGGCCAGGAGAGTCCGGTGGAGTCCTCATAGCCTTCTACTTATTGAGT
 TGGCTTGTGGATTATACTTCCCAGCATGAGCTCCTACGGAGAAAGGTGATCCCTGAGACA
 GAGCAGGCTGGTGTACTCAACTGGTCCGGTACCTCTGCACTCACTGGCTTGCCTAGGGCT
 CCTTGTCCCTCATGACAGTGATCGAAAAACAGGCACTCGGAATATGTTCAGCATTGCTCTG
 CTGTCATGGTGTGGCTCTGCTGGCAGTGGTGGACTCTCACCGTGGTAAGGCATGATGCT
 GAGCTGCGGGTACCTCACCTACTGAGGAGCCCTATGCCCTGAGCTG**TAA**CCCCACTCCAG
 GACAAGATAGCTGGACAGACTCTGAATTCCAGCTATCCGGATTGTACAGATCTCTCTGT
 GACTGACTTGTGACTGTCCTGTGGTTCTCCTGCCATTGCTTGTGTTGGAGGACATGA
 TGGGGGTGATGGACTGGAAAGAAGGTGCCAAAAGTTCCCTCTGTGTTACTCCATTAGAAA
 ATAAACACTTTAAATGATCAAAAAAAAAAAAAA

FIGURE 218

MLVTAYLAFVGLLASCLGLELSRCRAKPPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPY
LYKLYQHYYFLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTYSLCCLTKLS
QDYFVLLVGRALGGISTALLFSAFEAWYIHEHVERHDFFPAEWIPATFARA_AFWNHVLA
VAGVAEEAVASWIGLGPVAPFVAAIPLLALAGALALRNWGENYDRQRAFSRTCA
GGLRCLLSDRRVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAAS
LLGSSLYRIATSKRYHLQPMHLLSLAVLIVVFSLFMLTFSTSPGQESP
VESFIAFLIELACGLYFPSMSFLRRKVIPETEQAGV
LNWFRVPLHSLACLG
LLVLHDSDRKTGTRNMFSICSAVM
VMALLAVVGLFTVVRHDAELRV
VPSPTEEPYAPEL

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 41-55, 75-94, 127-143, 191-213, 249-270, 278-299,
314-330, 343-359, 379-394, 410-430

FIGURE 219

GCGACGCGCGGCCGGCGAGAGGAAACGCGGCCGGCCGGCCCTGGAG**ATG**
 GTCCCCGGCGCCGCGGGCTGGTGTCTCGTCTGGCTCCCGCGTCGCGCCTGGCCA
 CGGCTTCCGTATCCATGATTATTTGTACTTCAAGTGCTGAGTCCTGGGACATTGATACA
 TCTTCACAGGCCACACCTGCCAAGGACTTGGTGGTATCTTCACACAAGGTATGAGCAGATT
 CACCTTGTCCCCGCTGAACCTCCAGAGGCCTGCAGGGAACTCAGCAACGGTTCTCATCCA
 GGACCAAGATTGCTCTGGTGGAGAGGGGGGCTGCTCCTCTCCAAGACTCGGGTGGTCC
 AGGAGCACGGCGGGCGGGCGGTGATCATCTGACAACGCAGTTGACAATGACAGCTTCTAC
 GTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTTCTGCTCGG
 CCGAGACGGCTACATGATCCGCCCTCTGGAACAGCATGGCTGCCATGGCCATCATT
 CCATCCCAGTCAATGTCACCAGCATCCCCACCTTGAGCTGCTGCAACCGCCCTGGACCTTC
TGGTAGAAGAGTTGTCCCACATTCCAGCCATAAGTGACTCTGAGCTGGAAAGGGAAACCC
 AGGAATTTGCTACTTGAATTGGAGATAGCATCTGGGACAAGTGGAGCCAGGTAGAGGA
 AAAGGGTTGGCGTTGCTAGGCTGAAAGGAAGCCACACCACTGGCCTCCCTCCCCAGG
 GCCCCCAAGGGTGTCTCATGCTACAAGAAGAGGCAAGAGACAGGCCAGGGCTCTGGCTA
 GAACCCGAAACAAAAGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTACACT
 CACCTGGCTCCAGCCTCCCTACCCAGGGTCTGACAGTGACCTCACAGCAGTTGG
 AGTGGTTAAAGAGCTGGTGTGGGACTCAATAACCTCACTGACTTTAGCAATAAA
 GCTTCTCATCAGGGTGCAAAAAAAAAAAAAA

FIGURE 220

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532
><subunit 1 of 1, 188 aa, 1 stop
><MW: 21042, pI: 5.36, NX(S/T): 2
MVPGAAGWCCLVLWLPACVAAHGFRIHDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQ
IHLVPAEPPEACGELSNGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIISDNAVDNDSF
YVEMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISIPVNVTSIPTFELLQPPWTFW
```

Signal peptide:

amino acids 1-20

FIGURE 221

FIGURE 222

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76538
><subunit 1 of 1, 116 aa, 1 stop
><MW: 12910, pI: 6.41, NX(S/T): 1
MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGC
HCGILGGRGQPKDATDW
CCQTHDCCYDHLKTQGCGIYKDNNKSSIHCMDLSQRYCLMAVF
NVIYLENEDSE
```

Important features of the protein:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 1-24

N-glycosylation site.

amino acids 86-89

N-myristoylation sites.

amino acids 20-25, 45-50

Phospholipase A2 histidine active site.

amino acids 63-70

FIGURE 223

CTCGCTTCTCCTTCTGGATGGGGGCCAGGGGCCAGGAGAGTATAAAGGCATGTGGAG
GGTGCCCGGCACAACCAGACGCCAGTCACAGGCAGAGGCCCTGGG**ATG**CACCGGCCAGAGG
CCATGCTGCTGCTGCTCACGCTGCCCTCCTGGGGGCCACCTGGCAGGGAAGATGTAT
GCCCTGGAGGAGGCAAGTATTCAGCACCCTGAAGACTACGACCATGAAATCACAGGGCT
GCGGGTGTCTGTAGGTCTCCTGGTAAAAGTGTCCAGGTGAAACTGGAGACTCCTGGG
ACGTGAAACTGGGAGCCTAGGTGGAAATACCCAGGAAGTCACCCCTGCAGCCAGGCGAATAC
ATCACAAAAGTCTTGTGCCTTCCAAGCTTCCGGGTATGGTCATGTACACCAGCAA
GGACCGCTATTCTATTTGGAAAGCTTGTGGCATGCCAGATCTCCTGCCTACCCAGCCAAG
AGGGCAGGTGCTGGTGGCATCTATGCCAGTATCAACTCCTGGCATCAAGAGCATTGGC
TTTGAATGGAATTATCCACTAGAGGAGCCGACCACTGAGCCACCAGTTAACCTCACACTC
AGCAAACCTACCCGTGGGTGC**TAG**GGTGGGTATGGGCCATCCGAGCTGAGGCCATCTGT
GTGGTGGTGGCTGATGGTACTGGAGTAAGTGAGTCGGACGCTGAATCTGAATCCACCAATA
AATAAGCTCTGCAGAAAA

FIGURE 224

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19600, pI: 5.89, NX(S/T): 1
MHRPEAMLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSVQVK
LGDSWDVKLGALGGNTQEVTLQPGEYITKVFVAFQAFLRGMVMYTSKDRYFYFGKLDGQISS
AYPSQEGQVLVGIYGQYQLLGIKSIGFEWNYPLEEPTEPPVNLTYSANSPVGR
```

Signal peptide:

amino acids 1-22

FIGURE 225

GCTGAGCGTGTCGGTACGGGCTCTCCTGCCTCTGGCTCCAACGCAGCTCTGTGGCT
GAACGGGTGCTCATCACGGAACTGCTGGCTATGGAATACAGATGTGGCAGCTCAGGTAG
CCCCAAATTGCCCTGGAAGAATACATCATGTTTCGATAAGAAGAAATTGTAAGGATCCAGTT
TTTTTTTAACC GCCCCCCTCCCCACCCCCAAAAAAACTGTAAGATGCAAAAACGTAATAT
CCATGAAGATCTTACCTAGGAAGATTGATTTGCTGCGAATGCGGTGTTGGGATT
TATTTGTTCTGGAGTGTCTGCGTGGCTGGCAAAGAATAATGTTCAAAATCGGTCCATCT
CCAAGGGGTCCAATTTCCTGGGTGTCAGCGAGCCCTGACTCACTACAGTGCAGCTG
ACAGGGCTGTCACTGCAACTGGCCCTAACGCAAAGCAAAAGACCTAACGGACGACCTTGAA
CAATACAAAGG**ATG**GGTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTT
ATAGCCCCACTGTTACTGACAATGCTTCTGCCGAACGAGGGATGCCCTAACGGCTG
TAGGTGTGAAGGCAAATGGTATATTGTGAATCTCAGAAATTACAGGAGATAACCTCAAGTA
TATCTGCTGGTTGCTTAGGTTGTCCTCGCTATAACAGCCTCAAAACTAAGTATAAT
CAATTAAAGGGCTCAACCAGCTCACCTGGCTATACCTTGACCATAACCATAACGCAATAT
TGACGAAAATGCTTTAATGGAATACGCAACTCAAAGAGCTGATTCTTAGTCCAATAGAA
TCTCCTATTTCCTAACAAATACCTCAGACCTGTGACAAATTACGGAACCTGGATCTGTCC
TATAATCAGCTGCATTCTGGATCTGAAACAGTTGGGCTTGCGGAAGCTGCTGAGTT
ACATTACGGCTAACTCCCTGAGAACCATCCCTGTGCAATATTCCAAGACTGCCGCAACC
TGGAACTTTGGACCTGGGATATAACCGGATCCGAAGGTTAGCCAGGAATGCTTGTGGC
ATGATCAGACTCAAAGAACTTCACCTGGAGCACAATCAATTTCAGCTCAACCTGGCCCT
TTTCCAAGGTTGGTCAGCCTTCAGAACCTTACTTGCAGTGGATAAAATCAGTGTCAAG
GACAGACCATGTCCTGGACCTGGAGCTCCCTACAAAGGCTGATTATCAGGAATGAGATC
GAAGCTTCAGTGGACCCAGTGTGTTCCAGTGTGTCCTCGAATCTGCAGCGCCTCAACCTGG
TTCCAACAAGCTCACATTATTGGTCAAGAGATTGGATTCTGGATATCCCTCAATGACA
TCAGTCTGCTGGAAATATGGGAATGCAAGCAGAAATATTGCTCCCTGAAACTGGCTG
AAAAGTTAAAGGTCTAAGGGAGAATACAATTATCTGTGCCAGTCCAAAGAGCTGCAAGG
AGTAAATGTGATCGATGCAGTGAAGAACTACAGCATCTGTGGCAAAGTACTACAGAGAGGT
TTGATCTGCCAGGGCTCTCCAAAGCCGACGTTAAGCCCAAGCTCCCCAGGCCGAAGCAT
GAGAGCAAACCCCCCTTGGCCCCGACGGTGGAGCCACAGAGGCCAGAGACCAGATGC
TGACGCCGAGCACATCTTCCATAAAATCATCGCGGCGAGCGTGGCGTTTCTGTCCG
TGCTCGTCATCCTGCTGGTTATCTACGTGTCATGGAAAGCGGTACCCCTGCGAGCATGAAGCAG
CTGCAGCAGCGCTCCCTATGCGAAGGCACAGGAAAAAGAAAAGACAGTCCCTAAAGCAAAT
GAECTCCAGCACCCAGGAATTATGTAGATTATAAAACCCACCAACACGGAGACCAGCGAGA
TGCTGCTGAATGGGACGGGACCCCTGCACCTATAACAAATGGGCTCCAGGGAGTGTGAGGTA
TGAACCATTGTGATAAAAAGAGCTTAAAGCTGGAAATAAGTGGTCTTATTGAAC
TGGTGAATCAAGGGAACCGCGATGCCCTCCCTCCCTCTCAGCTTGGTGG
CAAGATCCTCTGTCCGTTAGTGCATTCAATAACTGGTATTTCCTCTACATACATA
ATCAACCCATTGAAATTAAATACCACAATGTAAGCTGAACTCCGGTTAATATAA
TACCTATTGTATAAGACCCCTTACTGATTCCATTAAATGTCGCATTGTTAAGATAAAACT
TCTTCATAGGTAAAAAAAAAAA

FIGURE 226

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77301
>subunit 1 of 1, 513 aa, 1 stop
><MW: 58266, pI: 9.84, NX(S/T): 4
MGFNVIRLLSGSAVALVIAPTVLLMLSSAERGCPKGCRCEGMVYCESQKLQEIPSSISAG
CLGLSLRYNSLQKLKYNQFKGLNQLTWLYLDHNHISNIDENAFNGIRRLKELILSSNRISYF
LNNTFRPVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHLRSNSLRTIPVRIFQDCRNLELL
DLGYNRIRSLARNVFAGMIRLKELHLEHNQFSKLNLAFFPRLVSIQONLYLQWNKISVIGQTM
SWTWSSLQRLDLSGNEIEAFSGPSVFQCVPNLQRNLDSNKLTFIGQEILDWSWISLNDISLA
GNIWECSRNICSLVNWLKSFKGLRENTIICASPKELQGVNVIDAVKNYSICGKSTTERFDLA
RALPKPTFKPKLPRPKHESKPPLPPTVGATEPGPETDADAEHISFHKIIAGSVALFLSVLVI
LLVIYVSWKRYPASMKQLOQRSLMRRHKKKRQLKQMTPSTQEFYVDYKPTNTETSEMLLN
GTGPCTYNKSGSRECEV
```

Important features of the protein:

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 420-442

N-glycosylation sites.

amino acids 126-129, 357-360, 496-499, 504-507

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 465-468

Tyrosine kinase phosphorylation site.

amino acids 136-142

N-myristoylation sites.

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

FIGURE 227

AGTTCTGAGAAAGAAGGAAATAAACACAGGCACCAAACCACTATCCTAAGTTGACTGTCCTT
 TAAATATGTCAAGATCCAGACTTTCACTGTCACCTCAGCGATCTAACGATAGGGATCTTG
 TGTTGCCGCTATTCCAGTTGGTGCTCTCGGACCTACCATGCGAAGAAGATGAAATGTGTGT
 AAATTATAATGACCAACACCCTAATGGCTGGTATATCTGGATCCTCCTGCTGGTTTG
 TGGCAGCTCTCTGTGGAGCTGTGGCCTCTGCCTCCAGTGCTGGCTGAGGAGACCCGA
 ATTGATTCTCACAGGCGCACCATGGCAGTTTGCTGTTGGAGACTGGACTCTATTATGG
 GACAGAAGCAGCTGTGAGTCCAACGTGGAATTCACCTCAAACCTCAAACCCCTGACCTAT
 ATCCTGTTCTGCTCCATGTTGGCCCTTAGGCTCCCCACCTCCATATGAAGAAATTGTA
 AAAACAACCTTGATTTAGGTGTGGATTATCAATTAAAGTATTAACGACATCTGTAATTCCA
 AACATCAAATTAGGAATAGTTATTCAGTTGGAAATGTCCAGAGATCTATTATATA
 GTCTGAGGAAGGACAATTGACAAAAGAATGGATGTTGGAAAAAAATTGGTCATGGAGATG
 TTTAAATAGTAAAGTAGCAGGCTTTGATGTGTCAGTGCTGTATCATACTTTATGCTACAC
 AACCAAATTAAATGCTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTT
 TCCATCACATTAGGACTCCACTGCAGTATACAGCACACCATTCTGCTTAAACTCTTC
 CTAGCATGGGTCCATAAAATTATAATTAAACAATAGCCCAAGCCGAGAATCCAACAT
 GTCCAGAACCCAGAACCAAGAGATAGTATTGAATGAAGGGTGAAGGGAGAGAGTAGGAAAAA
 GAAAAGTTGGAGTTGAAGGGTAAAGGATAATGAAGAGGAAAAGGAAAAGATTACAAGTCT
 CAGCAAAACAAGAGGTTTATGCCAACCTGAAGAGGAAGAAATTGTAGATAGAAGGTGA
 AGGAGATTGCTGAAGATATAGAGCACATATAATGCCAACACGGGAGAAAAGAAAATTCCC
 CTTTACAGTAATGAATGTGGCCTCCATAGTCATAGTGTCTCTGGAGCCTCAGGGCTTG
 GCATTTATTGCAGCATCATGCTAACCTCGGCATAGGTATCTGTTCCATGAGGACTGC
 AGAAGTAGCAATGAGACATCTCAAGTGGCATTTGGCAGTGGCCATCAGCAGGGGACAGA
 CAAAAACATCCATCACAGATGACATATGATCTCAGCTGACAAATTGTTGAACAAAACAAT
 AACATCAATAGATATCTAAAAA

FIGURE 228

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303
><subunit 1 of 1, 146 aa, 1 stop
><MW: 16116, pI: 4.99, NX(S/T): 0
MSRSRLFSVTSAISTIGILCLPLFQLVLSLPCCEEDEMVCNYNDQHPNGWYIWILLLLVLVA
· ALLCGAVVLCLQCWLRRPRIDSHRRTMAVFAVGDLDSIYGTEAAVSPTVGIGHLQTQTPDLYP
VPAPCFGPLGSPPPYEEIVKTT
```

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 52-70

FIGURE 229

GAGCGGAGTAAAATCTCCACAAGCTGGGAACAAACCTCGTCCCACCTCCCACCCACCGGCCT
 TTCTCCAGCTCGATCTGGAGGCTGCTTCGCCAGTGTGGGACGCAGCTGACGCCGCTTATT
 GCTCTCGCTCGTCGCCCGGCTCAGAAGCTCCGTGGCGGCCGACCGTGACGAGAACCC
 ACGGCCAGCTCAGTTCTCTTACTTTGGGAGAGAGAGAAAGTCAGATGCCCTTTAAACT
 CCCCTCTCAAAACTCATCTCCTGGGTGACTGAGTTAATAGAGTGGATAACACCTTGCTGAAG
 ATGAAGAATATAACATATTGAGGATATTTTTCTTTTTCAAGTCTGATTGTGGC
 TTACCTCAAGTTACCATTTTCAGTCAAGTCTGTTGTTGCTTCTCAGAA**ATG**TTTTTA
 CAATCTCAAGAAAAATATGTCCCAGAAATTGAGTTACTGTTGCTGTATTGGACTCATT
 TGGGGATTGATGTTACTGCACTATACTTTCAACAAACCAAGACATCAAAGCAGTGTCAAGTT
 ACGTGAGCAAATACTAGACTTAAGCAAAAGATATGTTAAAGCTCTAGCAGAGGAAAATAAGA
 ACACAGTGGATGTCGAGAACGGTGCTCTATGGCAGGATATGCGGATCTGAAAAGAACAAATT
 GCTGTCCTCTGGATGACATTGCAACGATTGGTGAAGCTGGAGAACAAAGTTGACTATAT
 TGTGTGAATGGCTCAGCAGCCAACACCAATGGTACTAGTGGGAATTGGTGCAGTAA
 CCACAAATAAAAGAACGAATGTCGCCCCAGTATCAGA**TAG**CAGTTGAAAATCACCTGTGC
 TGCTCCATCCACTGTTGATTATATCCTATGGCAGAAAAGCTTATAATTGCTGGCTTAGGAC
 AGAGCAATAACTTTACAATAAAAGCTCTACACATTCAAGGAGTATGCTGGATTGATGGAAC
 TCTAATTCTGTACATAAAATTAAAGTTATTGTTGCTTCAGGCAAGTCTGTTCAATG
 CTGTAATGTCCTAAAGAGAATTGTAACTGTTGATGTTGAGCAGATAGGTGAGT
 TTTGTATAAAATCTTGTGTTGAGATCAAGCTGAAATGAAAACACTGAAAACATGGATT
 ATTCTATAACACATTATTAAGTATATAACACGTTTGGACAAGTGAAGAATGTTAA
 TCATTCTGTCAATTGTTCTCAATAGATGTAACTGTTAGACTACGGCTATTGAAAAAATGTG
 CTTATTGTACTATATTGTTATTCCAATTATGAGCAGAGAAGGAAATATAATGTTGAAAA
 TAATGTTTGAAATCATGACCAAGAACATGTATTGATTTGACTATCCTCAGAATAACTGA
 AGGTTAATTATTGTATATTAAATTACACTTATAAGAGTATACTGAAATGGTAG
 CAGCCACTGTCATTACCTATCGTAAACATTGGGCAATTAAACAGCATTAAAATAGTT
 GTAAACTCTAATCTTACTTATTGAAGAATAAAAGATATTGATGAGAGTAACAATA
 AAGTATTGATGATTTCACATACATGAATGTTCATTTAAAGTTAATCCTTGAGTGTCT
 ATGCTATCAGGAAAGCACATTTCATATTGGGTTAATTGCTTTATTATATTGGTC
 TAGGAGGAAGGGACTTGGAGAATGGAACTCTTGAGGACTTAGCCAGGTGTATAATAAAA
 GGTACTTTGTGCTGCATTAAATTGCTGGAAAGTGTAAACATTATATTATAAGAGTATC
 CTTATGAAATTGAAATTGTATAACAGATGCATTAGATATTCAATTATATAATGCCAC
 TTAAGAACATTTAAATATAAACTATGAAGATTGACTATCTTTCAGGAAAAAGCT
 GTATATAGCACAGGGAAACCTAATCTGGGTAATTCTAGTATAAAACAAATTATACTTTAT
 TTAAATTCCCTGTAGCAAATCTAATTGCCACATGGTGCCTATATTCAAGTATTATT
 CTCTATAGTAACTGCTTAAGTGCAGCTAGCTTAGATTAGACTATATAGAATTAGATAT
 TGTATTGTTGTCATTATAATATGCTACCACATGTAGCAATAATTACAATTATTATAA
 TAAATATGTGAAATTGTTCATGAAAGACAGATTCCAAATCTCTCTTCTGT
 CTGCTACCTTATGTGAAGAAATTATGCCATTGCCAGGT

FIGURE 230

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648
><subunit 1 of 1, 140 aa, 1 stop
><MW: 15668, pI: 10.14, NX(S/T): 5
MFFTISRKNMSQKLSLLLLVFGLIWLMLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE
ENKNTVDVENGASMAGYADLKRTIAVLLDDILQRLVKLENKVDYIVVNGSAANTTNGTSGNL
VPVTTNKRTNVSGSIR
```

Important features of the protein:

Signal peptide:

amino acids 1-26

FIGURE 231

CGCGGCCGGCCGCCGGGTGAGCGTGCCGAGGCGCTGTGGCGCAGGCTTCCAGCCCCAC
CATCCGTGGCCCTGCTGCTGCTGGCCGTAGTGGGCCAGACAACCGGCCATGCT
 TCCCCTGGGTGCCAATGCGAGGTGGAGACCTTCGGCCTTTCGACAGCTTCAGCCTGACTCGG
 GTGGATTGTAGCGGCCCTGGGCCACATCATGCCGGTGCCCATCCCTCTGGACACAGCCA
 CTTGGACCTGTCCTCCAACC GGCTGGAGATGGTGAATGAGTCGGTGTGGCGGGGCCGGCT
 ACACGACGTTGGCTGGCCTGGATCTCAGCCACAACCTGCTCACCAAGCATTCAACCACTGCC
 TTCTCCGCCTCGTACCTGGAGTCGCTTGACCTCAGCCACAATGGCCTGACAGCCCTGCC
 AGCCGAGAGCTTCACCAAGCTCACCCCTGAGCGACGTGAACCTTAGCCACAACCAGCTCCGG
 AGGTCTCAGTGTCTGCCTTCACGACGACAGTCAGGGCCGGCACTACACGTGGACCTCTCC
 CACAACCTCATTACCGCCTCGTGCCCCACCCACGAGGGCCGGCTGCCTGCGCCCACCAT
 TCAGAGCCTGAACCTGGCCTGAAACCGCTCCATGCCGTGCCAACCTCCGAGAGACTTGCCCC
 TCGCCTACCTGAGCCTGGATGGAACCCCTAGCTGTCAATTGGTCCGGTGCCTCGCGGG
 CTGGGAGGCCTTACACACCTGCTCTGCCAGCCTGCAGAGGCTCCCTGAGCTGGCGCCAG
 TGGCTCCGTGAGCTACCGGGCTGCAGGTCTGGACCTGTCGGCAACCCAAAGCTTAAC
 GGGCAGGAGCTGAGGTGTTTCAGGCCTGAGCTCCCTGCAGGAGCTGGACCTTCGGCACC
 AACCTGGTCCCCCTGCCTGAGGCCTGCTCCCTCACCTCCGGCACTGCAGAGCGTCAGCGT
 GGGCAGGATGTGCGGTGCCGGCCTGGTGCAGGGCACCTACCCCGGAGGCCTGGCT
 CCAGCCCCAAGGTGCCCTGCACTGCGTAGACACCCGGAAATCTGCTGCCAGGGGCCACC
 ATCTTG**TGACA**AAATGGTGTGGCCAGGGCACATAACAGACTGCTGTCTGGCTGCCTCAG
 GTCCCAGTAACCTATGTTCAATGTGCCAACACCAAGTGGGAGCCCGAGGCCTATGTGGCA
 GCGTCACCACAGGAGTTGTGGGCCTAGGAGAGGCTTGGACCTGGAGGCCACACCTAGGAGC
 AAAGTCTCACCCCTTGTCTACGTTGCTCCCCAAACCATGAGCAGAGGGACTTCGATGCCA
 AACCAACTCGGGTCCCCCTGCCTTCCCTCCCCACTTATCCCCAAAGTGCCTTCCCTCAT
 GCCTGGGCCGGCCTGACCCGCAATGGCAGAGGGTGGGGACCCCTGCTGCAGGGCAGA
 GTTCAGGTCACTGGCTGAGTGTCCCCATGGCCAGTCACTCAGGGCGAGTT
 TCTTTCTAACATAGCCCTTCTTGCATGAGGCCATGAGGCCCTTCATCCTTCTAT
 TTCCTAGAACCTTAATGGTAGAAGGAATTGCAAAGAATCAAGTCCACCCCTCTCATGTGAC
 AGATGGGAAACTGAGGCCTTGAGAAGAAAAAGGCTAATCTAAGTCTCTGCCAGTGGC
 ATGACTGGAGCACAGCTCTGCCTCCAGCCGGACCCAAATGCACTTCTGTCTCTCTA
 ATAAGCCCCACCCCTCCCCGCCTGGCTCCCCCTGCTGCCCTGCCATTAGCACA
 GGAGTAGCAGCAGCAGGACAGGCAAGAGCCTACAAGTGGACTCTGGCCTCTGACCAGCT
 GTGCCGCATGGCTAAGTCACTCTGCCCTCGGAGCCTGGAAGCTAGGGCACATTGGTT
 CCAGCCTAGCCAGTTCTCACCCCTGGGTGGGGCCCCAGCATCCAGACTGGAAACCTACC
 CATTTCCCCCTGAGCATCCTCTAGATGCTGCCCAAGGAGTTGCTGCAGTTCTGGAGCCTCA
 TCTGGCTGGATCTCAAGGGCCTCCGGATTCAAGTCCCCACTGCCCTGAGCACGACAGC
 CCTCTTACCCCTCCAGGAATGCCGTGAAAGGAGACAAGGTCTGCCGACCCATGTCTATGC
 TCTACCCCAAGGCAGCATCTCAGCTTCCGAACCCCTGGCTTTCTTAGTCTTCAATTAA
 TAAAAGTTGGCTTTAACGGAGTGCACTTCAACCGGCCTCCCTACCCCTGCTGGC
 CGGGGATGGAGACATGTCATTGTAAGCAGAAAAGGTTGCATTGTTCACTTTGTAAT
 ATTGTCCTGGGCCTGTTGGGGAGCTGGCATTAGTGGCCACATGGCATTG
 AGGGCTGGCCCCACAGAGACCCACAGGGCAGTGAGCTGTCTCCCCACCTGCCAGC
 CCATCATCTAACCGGTCTTGATTAAACACTATAAAAGGTTAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAA

FIGURE 232

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77652
><subunit 1 of 1, 353 aa, 1 stop
><MW: 37847, pI: 6.80, NX(S/T): 2
MPWPLLLLAVSGAQQTTRPCFPGCQCEVETFGLFDSFSLTRVDCSGLGPHIMPVPIPLDTAH
LDLSSNRLEMVNESVLAGPGYTTLAGLDLSHNLLTSISPTAFSRLRYLESLDLSHNGLTALP
AESFTSSPLSDVNLSHNQLREVSVAFTTHSQGRALHVDSLHNLIHRLVPHPTRAGLPAPTI
QSLNLAWNRLHAVPNLRDPLRYLSDLGNPLAVIGPGAFAGLGGLTHLSLASLQRIPELAPS
GFRELPGLQVLDSLGNPKLNWAGAEVFSGLSSLQELDLSGTNLVPLPEALLLHLPALQSVSV
GQDVRCRRLVREGTYPRRPGSPPKVPLHCVDTRESAARGPTIL
```

Signal peptide:

amino acids 1-16

Transmembrane domains:

amino acids 215-232, 287-304

FIGURE 233

GATGGCGCAGCCACAGCTTCTGTGAGATTGATTCCTCCCCAGTTCCCCTGTGGGTCTGAGG
 GGACCAGAAGGGTGAGCTACGTTGGCTTCTGGAAGGGGAGGGCTATATGCGTCAATTCCCCA
 AAACAAGTTTGACATTCCCCTGAAATGTCATTCTATCTATTCACTGCAAGTGCCTGCT
 GTTCCAGGCCTTACCTGCTGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGC
 CACGACCTGTGCCACCAACTCGCACTCAGACTCTGAACCTCAGACCTGAAATCTCTTCAC
 GGGAGGCTTGGCAGTTTCTACTCCTGTGGTCTCCAGATTCAAGGCCTAAGATGAAAGCC
 TCTAGTCTGCCTTCAGCCTCTCTGCTGCCTTATCTCCTATGGACTCCTCCACTGG
 ACTGAAGACACTCAATTGGAAAGCTGTGTGATGCCACAAACCTCAGGAAATACGAAATG
 GATTTCTGAGATAACGGGGCAGTGTGCAAGCCAAGATGAAACATTGACATCAGAAATCTTA
 AGGAGGACTGAGTCTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCCATT
 GCTAAGACTCTATCTGGACAGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCC
 GGAAGATCAGCAGCCTGCCAATTCTTCTTACCATCAAGAAGGACCTCCGGCTCTCAT
 GCCCACATGACATGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCA
 CTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGCTTGGGGAACTAGACATTCTTC
 TGCAATGGATGGAGGAGACAGAATAGGAGGAAAGTGTGCTGCTGCTAAGAATATTGAGGT
 CAAGAGCTCCAGTCTCAATACCTGCAAGAGGAGGCATGACCCAAACCACCATCTCTTACT
 GTACTAGTCTGTGCTGGTCACAGTGTATCTTATTGCATTACTGCTTGCATGAT
 TGTCTTATGCATCCCCATCTTAATTGAGACCATACTGTATAAGATTTGTAAATATCTT
 TCTGCTATTGGATATTTATTAGTTAATATATTATTATTATTTGCTATTAAATGTATTT
 ATTTTTACTGGACATGAAACTTAAAAAAATCACAGATTATTTATAACCTGACTAG
 AGCAGGGTGTATTTATACAGTAAAAAAAAACCTGTAAATTCTAGAAGAGTGGCT
 AGGGGGTTATTCATTGTATTCAACTAAGGACATATTACTCATGCTGATGCTCTGTGAGA
 TATTGAAATTGAACCAATGACTACTTAGGATGGGTGTGGAATAAGTTGATGTGGAATT
 GCACATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCATAATTGTGTAT
 CTTCCAGCCAGGAATCCTACACGGCCAGCATGTATTCTACAAATAAGTTTCTTGCATA
 CCAAAAAAAAAAAAAAAA

FIGURE 234

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500
><subunit 1 of 1, 261 aa, 1 stop
><MW: 29667, pI: 8.76, NX(S/T): 0
MRQFPKTSFDISPEMSFSIYSILQVPAVPGLTCWALTAEPGWGQNKGATTCATNSHSDSELRP
EIFSSREAWQFFLLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNL
QEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTP
DHYTLRKISSLANSFLTICKDLRLSHAHMTCHCCEEAMKKYSQILSHFEKLEPQAAVKALG
ELDILLQWMEETE
```

Important features of the protein:

Signal peptide:

amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 192-195, 225-228

N-myristoylation sites.

amino acids 42-47, 46-51, 136-141

FIGURE 235

CCGTTATCGTCTTGCCTACTGCTGAATGTCCGTCCGGAGGAGGAGGGCTTGGC
 CTGACCCAGAGATGGCCCCGAGCGAGCAAATTCTACTGTCCGGCTGCGCGCTACCGTGG
 CGAGCTAGCAACCTTCCCCTGGATCTCACAAAAACTCGACTCAAATGCAAGGAGAAGCAG
 CTCTGCTCGGTTGGGAGACGGTGCAAGAGAACTGCCCCCTATAAGGGAAATGGTGCAC
 GCCCTAGGGATCATTGAAGAGGAAGGCTTCTAAAGCTTGGCAAGGAGTGACACCCGCCAT
 TTACAGACACGTAGTGTATTCTGGAGGTCGAATGGTCACATATGAACATCTCCGAGAGGTTG
 TGTTGGCAAAAGTGAAGAGATGAGCATTATCCCCTTGGAAATCAGTCATTGGAGGGATGATG
 GCTGGTGTATTGGCCAGTTTAGCCAATCCAACGTGACCTAGTGAAGGTTCAGATGCAAAT
 GGAAGGAAAAGGAAACTGGAAGGAAACCATTGCGATTCTGTGGTGTACATCATGCATTG
 CAAAAATCTTAGCTGAAGGAGGAATACGAGGGCTTGGCAGGCTGGTACCAATATAACAA
 AGAGCAGCACTGGTGAATATGGGAGATTAAACCACTTATGATACTGAAACACTACTTGGT
 ATTGAATACACCACTTGAGGACAATATCATGACTCACGGTTATCAAGTTATGTTCTGGAC
 TGGTAGCTTCTATTCTGGAACACCAGCCGATGTCATCAAAAGCAGAATAATGAATCAACCA
 CGAGATAAACAGGAAGGGACTTTGTATAAATCATGACTGACTGCTTGATTAGGCTGT
 TCAAGGTGAAGGATTCATGAGTCTATAAAAGGTTTACCATCTGGCTGAGAATGACCC
 CTTGGTCAATGGTGTCTGGCTTACTTATGAAAAAAATCAGAGAGATGAGTGGAGTCAGTCCA
 TTTTAA

FIGURE 236

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77568
><subunit 1 of 1, 323 aa, 1 stop
><MW: 36064, pI: 9.33, NX(S/T): 1
MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMGEAALARLGDGA
RESAPYRGMVRTALGIIEEGFLKLWQGVTPAIYRHVVYSGGRMVTYEHLREVVFGKSEDEH
YPLWKSVIGGMMAGVIGQFLANPTDLVKVQMQMEGKRKLEGKPLRFRGVHHAFAKILAEGGI
RGLWAGWVPNIQRAALVNMGDLTTYDTVKHYLVLNTPLEDNIMTHGLSSLCGLVASILGTP
ADVIKSrimnQPRDKQGRGLLYKSSTDCLIQAVQGEGFMSLYKGFLPSWLRMTPWSMVFWLT
YEKIREMSGVSPF
```

Transmembrane domains:

amino acids 25-38, 130-147, 233-248

FIGURE 237

CGGACGCGTGGCGCGGGACGCCGGCAGGGTTGGCGCAGCAGTCTCCTCCTGCAGCG
 GCCTGAAGTCGGCGTGGCGTTGAGGAAGCTGGGATAACAGCATTAAATGAAAAATTATGC
 TTAAGAAGTAAAA**ATG**GCAGGCTCCTAGATAATTCGTTGGCCAGAATGTGAATGTATTG
 ACTGGAGTGAGAGAAGAAAATGCTGTGGCATCTGGTGTGCAGGTATATTGTTTTACAGGC
 TGGTGGATAATGATTGATGCAGCTGTGGTGTACCTAAGCCAGAACAGTTGAACCATGCC
 TCACACATGTGGTGTATTTCACATTGGCTTCTCATGATAAAATGCTGTATCCAATGCTC
 AGGTGAGAGGTGATAGCTATGAAAGCGGCTGTTAGGAAGAACAGGTGCTCGAGTTGGCTT
 TTCATTGGTTCATGTTGATGTTGGGTCACTTATTGCTCCATGTGGATTCTTTGGTGC
 ATATGTTACCCAAAATACTGATGTTATCCGGACTAGCTGTGTTTTCAAATGCACTTA
 TATTTTTAGCACTCTGATCTACAAATTGGAAGAACCGAAGAGCTATGGACC**TGA**GATCAC
 TTCTTAAGTCACATTTCTTTGTTATTCGTTAGATAGGTTTTATCTCTCAGT
 ACACATTGCCAAATGGAGTAGATTGTACATTAATGTTGTTCTTACATTTATGTT
 TGAGTTTGAAATAGTTATGAAATTCTTATTTTCATTGCATAGACTGTTAATATGTA
 TATAATACAAGACTATATGAATTGGATAATGAGTATCAGTTTTATTCTGAGATTAGAA
 CTTGATCTACTCCCTGAGCCAGGGTTACATCATCTGTCATTTAGAAGTAACCACTCTGT
 CTCTCTGGCTGGCACGGTGGCTCATGCCTGTAATCCCAGCAGTGGGAGGCCAGGG
 CCGATTGCTTGAGGTCAAGTGGTGGACAGCAGCCTGGCAACATGGCGAAACCCATCTACT
 AAAAATACAAAAATTAGCCAGGCATGGTGGTGGCTGTAATCCCAGCTACCTGGGAGGC
 TGAGGCAGGAGAATCGCTGAACCCGGGGGGCAGAGGTTGCAGTGAGCTGAGTTGCGCCAC
 TGCACCTAGCCTGGGGAGAAAGTGAACACTCCCTCTCAAAAAAAAGACCACTCTCAGTATC
 TCTGATTTCTGAAGATGTACAAAAAAATATAGCTTCATATCTGGAATGAGCACTGAGCCA
 TAAAAGGTTTCAGCAAGTTGTAACTTATTTGGCCTAAAAATGAGGTTTTGGTAAAGA
 AAAAATATTGTTCTATGTATTGAAGAAGTGTACTTTATATAATGATTTTAAATGCC
 AAAGGACTAGTTGAAAGCTTCTTTAAAAAGAATTCTCTAATATGACTTATGTGAGAA

FIGURE 238

MAGFLDNFRWPECECIDWSERRNAVASVVAGILFFTGWWIMIDAADVYPKPEQLNHAFHTCG
VFSTLAFFMINAVSNAQVRGDSYESGCLGRTGARVWLFIGFMLMFGSLIASMWILFGAYVTQ
NTDVYPGLAVFFQNALIFFSTLIYKFGRTEELWT

Important features:

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 23-42 (type II), 60-80, 97-117, 128-148

FIGURE 239

GTTGATGGCAAACCTCCTCAAAGGAGGGCAGAGCCTGCGCAGGGCAGGAGCAGCTGGCCA
 CTGGCGGCCCGCAACACTCCGTCTCACCTCTGGGCCACTGCATCTAGAGGAGGGCCGTCT
 GTGAGGCCACTACCCCTCCAGCAACTGGGAGGTGGACTGTCAGAAGCTGGCCAGGGTGGT
 GGTCACTGGGTCAAGGGACCTACGGCACCTGCTGGACCACCTCGCCTCTCCATCGAAGCAG
 GGAAGTGGGAGCCTCGAGCCCTCGGGTGGAAAGCTGACCCCAAGCCACCCTCACCTGGACAG
GATGAGAGTGTCAAGGTGTGCTCGCCTCGCCCTCATCTTGCCATAGTCACGACATGGA
 TGTTTATTCAAGCTACATGAGCTTCAGCATGAAAACCATCCGTCTGCCACGCTGGCTGGCA
 GCCTCGCCCACCAAGGAGATCCAGGTTAAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCC
 AGCCAACACTTGCCTTAAAATCTGCAGTGGGCCGCAAACGTCGTGGCCCTACTATGT
 GCTTGAAAGACCGCATGATCATGAGTCCTGTGAAAAACAATGTGGCAGAGGCCTAACATC
 GCCCTGGTGAATGGAACCACGGGAGCTGTGCTGGACAGAAGGCATTTGACATGTACTCTGG
 AGATGTTATGCACCTAGTGAAATTCTTAAAGAAATTCCGGGGGTGCACTGGTGCTGGTGG
 CCTCCTACGACGATCCAGGGACCAAAATGAACGATGAAAGCAGGAAACTCTCTGACTTG
 GGGAGTTCCCTACGCAAAACAACGGGCTTGGAGCAGTTCTAAAGAACAGCCAGACACAAACAAATACG
 AGGGATGGCCAGAGCTGGAGATGGAGGGCTGCATGCCCGAAGCCATTTAGGGTGGC
 TGTGGCTTCCCTAGCCAGGGCCTGAAGAAGCTCCTGCCTGACTTAGGAGTCAGAGCCCG
 GCAGGGGCTGAGGAGGGAGCAGGGGTGCTGGTGGAAAGGTGCTGCAGGTCTGCACGC
 TGTGTCGCGCCTCTCCTCGGAAACAGAACCCCTCCCACAGCACATCCTACCCGGAAGACC
 AGCCTCAGAGGGCCTCTGGAACCGAGCTGTGAGAGAATGGGTGCTTCGTCAAGGG
 ACTGCTGACGGCTGGCCTGAGGAAGGACAAACTGCCAGACTTGAGCCAATTAAATTAA
 TTTTGCTGGTTTGAAAAAAAAAAAAAAAAAAAAA

FIGURE 240

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59814
<subunit 1 of 1, 224 aa, 1 stop
<MW: 24963, pI: 9.64, NX(S/T): 1
MRVSGVLRLALIFAIVTTWMFIRSYMSFSMKTIRLPRWLAASPTKEIQVKKYKCGLIKPCP
ANYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNNTTGAVLGQKAFDMYSG
DVMHLVKFLKEIPGGALVLVASYDDPGTKMNDESRKLFDLGSYAKQLGFRDSWVFIGAKD
LRGKSPFEQFLKNSPDTNKYEGWPELLEMEGCMPPKPF
```

Important features:

Signal peptide:

amino acids 1-15

ATP/GTP-binding site motif A (P-loop).

amino acids 184-191

N-glycosylation site.

amino acids 107-110

FIGURE 241

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTGTCTGGGAT
 CCAGAAACCATGATAACCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGAGACA
 GCAAGAGAAGCAGAGATAAACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTCTC
 TCACTCCCTCCCTCCCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAATTCCCAGTCCC
 CTGCACCCCTTCCTGGGACACT**ATG**TTGTTCTCCGCCCTGCTGGAGGTGATTGGATCC
 TGGCTGCAGATGGGGTCAACACTGGACGTATGAGGGCCACATGGTCAGGACCATTGCCA
 GCCTCTTACCCCTGAGTGTGGAAACAATGCCAGTCGCCATCGATATTAGACAGACAGTGT
 GACATTGACCCTGATTGCCTGCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGC
 CTTGGACCTGCACAACAATGCCACACAGTGCAACTCTCTGCCCTTACCCGTATCTG
 GGTGGACTTCCCCGAAAATATGTAGCTGCCAGCTCACCTGCACTGGGTCAAAAGGATC
 CCCAGGGGGTCAGAACACCAGATCAACAGTGAAAGCCACATTGAGCTCCACATTGTAC
 ATTATGACTCTGATTCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCTCAGGGCTGGCT
 GTCCTGGGCATCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAAACACATTCTGAG
 TCACTTGCATGAAGTCAGGCATAAAGATCAGAACAGCTCAGTGCTCCCTAACCTAACAGAG
 AGCTGCTCCCCAACAGCTGGGCAGTACTCCGCTACAATGGCTCGCTCACAACTCCCCCT
 TGCTACCAAGAGTGTGCTCTGGACAGTTTATAGAAGGTCCCAGATTCAATGAAACAGCT
 GGAAAAGCTTCAGGGACATTGTTCTCACAGAACAGGAGCCCTTAAGCTCTGGTACAGA
 ACTACCGAGCCCTTCAGCCTCTCAATCAGCGATGGTCTTGCTTTCATCCAAGCAGGA
 TCCTCGTATACCACAGGTGAAATGCTGAGTCTAGGTGTAGGAATCTGGTGGCTGTCTG
 CCTTCTCCTGGCTGTTATTCATTGCTAGAAAGATTGGAAGAACAGGCTGGAAAACGAA
 AGAGTGTGGCTTCACCTCAGCACACAAGCCACGACTGAGGCA**TAA**ATTCTCTCAGATACCA
 TGGATGTGGATGACTCCCTCATGCCTATCAGGAAGCCTCTAAATGGGTGAGGATCTG
 GCCAGAAACACTGTAGGAGTAGTAAGCAGATGTCCTCCTCCCTGGACATCTTAGAGAG
 GAATGGACCCAGGCTGTCATTCCAGGAAGAACACTGCAGAGCCTCAGCCTCTCAAACATGTA
 GGAGGAAATGAGGAATCGCTGTGTTAATGCAGAGANCAAACCTGTTAGTTGCAGGG
 GAAGTTGGATATACCCCAAAGTCCTACCCCTCACTTATGCCCTTCCCTAGATA
 TACTGCGGGATCTCTCCTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTGATCAATA
 TATTGGAAATTAAAGTTCTGACTTT

FIGURE 242

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812
><subunit 1 of 1, 337 aa, 1 stop
><MW: 37668, pI: 6.27, NX(S/T): 1
MLFSALLLEVIWILAADGGQHWTYEGPHQDHWPASYPECGNNAQSPIDIQTDSTFDPDLP
ALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQ
INSEATFAELHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRH
KDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTL
FSTEEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYF
IARKIRKKRLENRKSVVFTSAQATTEA
```

Important features of the protein:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 291-310

N-glycosylation site.

amino acids 213-216

Eukaryotic-type carbonic anhydrases proteins

amino acids 197-245, 104-140, 22-69

FIGURE 243

FIGURE 244

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSSLIPLTQM
LTLPDLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGTILSSEE
LPQIFTSLIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGT PAGR LPTPSG
TDDDFAVTTPAGIQRSTHAI EATTE SANGIQ

Signal peptide:

amino acids 1-16

FIGURE 245

4000 3500 3000 2500 2000 1500 1000

GGAGAGAGGCGCGCGGGTGAAGGCGCATTGATGCAGCCTGCGGCCGCTCGAGCGCGCG
 GAGCCAGACGCTGACCACGTTCTCTCCTCGGTCTCCTCCGCCTCAGCTCCGCGCTGCCCG
 GCAGCCGGAGCC**ATG**CGACCCCAGGGCCCCGCCCTCCCGCAGCGGCTCCGCGGCCCTCC
 TGCTGCTCCTGCTGCTGCAGCTGCCGCGCCGTGAGCGCCTCTGAGATCCCCAAGGGGAAG
 CAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGACCTGTATAATGGAATGTGCTTACAAGG
 GCCAGCAGGAGTGCCTGGTCGAGACGGAGCCCTGGGCCAATGTATTCCGGTACACCTG
 GGATCCCAGGTGGATGGATTCAAAGGAGAAAAGGGGAATGTCAGGGAAAGCTTGAG
 GAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCAATTGATAGATCT
 TGGGAAAATTGCGGAGTGTACATTACAAAGATGCGTTCAAATAGTGCTCTAACAGAGTTGT
 TCAGTGGCTCACTCGGCTAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTCACATTC
 AATGGAGCTGAATGTTCAAGGACCTCTTCCCATTGAAGCTATAATTATTGGACCAAGGAAG
 CCCTGAAATGAATTCAACAATTAAATATTCACTCGCACTTCTGTGGAAGGACTTGTGAAG
 GAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGTTGGCACTGTTCAAGATTACCAAAA
 GGAGATGCTTCACTGGATGGAATTCAAGTTCTCGCATCATTATTGAAGAACTACCAAA**TA**
AATGCTTAATTTCAATTGCTACCTCTTTTATTATGCCTGGAATGGTCACTTAAAT
 GACATTAAATAAGTTATGTATACATCTGAATGAAAGCAAAGCTAAATATGTTACAGA
 CCAAAGTGTGATTCACACTGTTAAATCTAGCATTATTCACTTCAATCAAAGT
 GGTTCAATATTTTTAGTTGTTAGAATACTTCTTCATAGTCACATTCTCAACCTA
 TAATTGGAATATTGTTGTTAGTTCTTAGTATAGCATTAAAAAAATA
 TAAAAGCTACCAATCTTGTACAATTGTAAGAATTTTTATATCTGTTAAAT
 AAAAATTATTCCAACA